

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3296.03 Seconds
(without alignments)
10265.033 Million cell updates/sec

Title: US-10-070-532-5

Perfect score: 1133

Sequence: 1 atggagccctcagccacccc.....tcctgaccatcggtccccgg 1133

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	715.2	63.1	1740	11	BC035686	BC035686 Homo sapi
c 2	701.4	61.9	886	13	BX433093	BX433093 BX433093
c 3	659.2	58.2	899	13	BX433092	BX433092 BX433092
4	561.4	49.5	753	29	AY420885	AY420885 Homo sapi
5	530.4	46.8	3470	11	AK048781	AK048781 Mus muscu
6	530.4	46.8	3729	11	AK038551	AK038551 Mus muscu
7	519.8	45.9	1790	11	BC035858	BC035858 Homo sapi
8	519.4	45.8	3153	11	AK079572	AK079572 Mus muscu
c 9	504.4	44.5	790	14	CF147830	CF147830 AGENCOURT
10	474.2	41.9	750	29	AY420886	AY420886 Pan trogl
11	472	41.7	1001	9	AL535838	AL535838 AL535838
12	468.6	41.4	726	29	AY420887	AY420887 Mus muscu
13	393.2	34.7	993	12	BM926746	BM926746 AGENCOURT
14	374.6	33.1	543	13	BX119589	BX119589 BX119589
15	367	32.4	788	14	CF147829	CF147829 AGENCOURT
16	329.2	29.1	382	12	BQ042116	BQ042116 sheep1 Sh
c 17	296	26.1	525	12	BI133700	BI133700 UI-M-BH3-
18	285.4	25.2	635	12	BM939496	BM939496 UI-M-BH3-
19	278.4	24.6	520	13	BQ269289	BQ269289 ik23f12.y
20	265.8	23.5	627	10	BB632359	BB632359 BB632359
21	265.4	23.4	599	12	BM933820	BM933820 UI-M-BH3-
22	263.2	23.2	611	13	BY723922	BY723922 BY723922
23	249	22.0	892	13	BX409735	BX409735 BX409735
24	216.8	19.1	477	12	BM087401	BM087401 500158 MA
25	202.4	17.9	662	10	BB632883	BB632883 BB632883
c 26	198.4	17.5	625	13	BQ285933	BQ285933 ik23f12.x
27	198.2	17.5	1073	12	BM920548	BM920548 AGENCOURT
28	197.6	17.4	505	10	BB651179	BB651179 BB651179
29	196.8	17.4	245	12	BI976482	BI976482 485407 MA
30	186.2	16.4	464	13	BY239887	BY239887 BY239887
31	175.4	15.5	444	14	R55704	R55704 yg88h10.rl
c 32	165.8	14.6	703	29	CE375359	CE375359 tigr-gss-
33	163.2	14.4	1290	29	AY411591	AY411591 Homo sapi
34	162	14.3	721	29	CE235359	CE235359 tigr-gss-
35	157.8	13.9	1296	29	AY411593	AY411593 Mus muscu
c 36	156.2	13.8	1013	9	AL535837	AL535837 AL535837
37	147.2	13.0	768	13	BX109847	BX109847 BX109847
38	133	11.7	257	10	AW427900	AW427900 64510 MAR
c 39	127.2	11.2	1005	28	CC212654	CC212654 CH261-75F
c 40	127.2	11.2	1058	28	CC297061	CC297061 CH261-177
c 41	122.4	10.8	1194	28	CC279941	CC279941 CH261-24C
42	120.2	10.6	526	29	CG978334	CG978334 CH240_169
43	119	10.5	1113	29	AY420480	AY420480 Homo sapi
44	117.8	10.4	1100	29	AY420481	AY420481 Pan trogl
45	108.8	9.6	1113	29	AY420482	AY420482 Mus muscu

ALIGNMENTS

RESULT 1
BC035686

LOCUS BC035686 1740 bp mRNA linear HTC 20-SEP-2002

DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone IMAGE:5750551, mRNA.

ACCESSION BC035686

VERSION BC035686.1 GI:23242909

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1740)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov>/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 79 Row: m Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557636
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers

source 1. .1740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750551"
/tissue_type="Lung, Spleen, fetal, pooled"

/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Vector: pcMV-SPORT6"

ORIGIN

Query Match 63.1%; Score 715.2; DB 11; Length 1740;
Best Local Similarity 83.3%; Pred. No. 4.8e-139;
Matches 906; Conservative 0; Mismatches 3; Indels 179; Gaps 1;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 506 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 565

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db 566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGCGATTATCTG 625

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
Db 626 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 685

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 686 CTGGTGGCAACACGCTG----- 703

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 704 ----- 703

Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGGCCATGCCCTGCAAG 360
Db 704 ----- 703

Qy 361 GTCATCCCCTATCTACAGGCTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 704 -----GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480
Db 747 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 806

Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGCTGGCCATCATGGTCCCCAGGCT 540
Db 807 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGCTGGCCATCATGGTCCCCAGGCT 866

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 926

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db 927 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 986

Qy 661 ATTGTACACTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Db 987 ATTGTACACTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 1046

Qy	721 AAGCTCTGGGCCGCCCCAGATCCCCGGCACCAACCTCAGCACTGGTGC GGAACTGGAAGCGC	780
Db	1047 AAGCTCTGGGCCGCCCCAGATCCCCGGCACCAACCTCAGCACTGGTGC GGAACTGGAAGCGC	1106
Qy	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	1107 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	1166
Qy	841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1226
Qy	901 ATGGTGGTGCTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	1227 ATGGTGGTGCTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	1286
Qy	961 AAGAGGGTGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCCTGCTTC	1020
Db	1287 AAGAGGGTGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCCTGCTTC	1346
Qy	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1347 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1406
Qy	1081 CTCAGTGG 1088	
Db	1407 CTCAGTGG 1414	

RESULT 2

BX433093/c

LOCUS BX433093 886 bp mRNA linear EST 15-MAY-2003
 DEFINITION BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF013YE04 3-PRIME, mRNA sequence.
 ACCESSION BX433093
 VERSION BX433093.1 GI:30779168
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 886)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 151.r For
 more information about this cluster, see
<http://www.genoscope.cns.fr/>
[cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r).
 Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_2.

FEATURES	Location/Qualifiers
source	1. .886 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DF013YE04" /tissue_type="FETAL BRAIN" /dev_stage="fetal" /clone_lib="Homo sapiens FETAL BRAIN" /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN	
	Query Match 61.9%; Score 701.4; DB 13; Length 886; Best Local Similarity 99.0%; Pred. No. 2.8e-136; Matches 705; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy	377 AGGCTGTGTCCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGT 436
Db	745 AGGCTGTGTCCCGTGTCAAGTGACAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGT 686
Qy	437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCC GGCGGGCCGTGGCTCCATCC 496
Db	685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCC GGCGGGCCGTGGCTCCATNC 626
Qy	497 TGGGCATCTGGCTGTGCGCTGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
Db	625 TGGGCATCTGGCTGTGCGCTGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATGCA 566
Qy	557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCAGTCTGTGATGAACGCT 616
Db	565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCAGTCTGTGATGAACGCT 506
Qy	617 GGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGG 676
Db	505 GGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGG 446
Qy	677 CCCCCACTGGGCCTCATGCCATGCCATTTCAGATATTCCGCAAGCTGGGGCCGCC 736
Db	445 CCCCCACTGGGCCTCATGCCATGCCATTTCAGATATTCCGCAAGCTGGGGCCGCC 386
Qy	737 AGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGCCCTCAGACCAGCTGG 796
Db	385 AGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGCCCTCAGACCAGCTGG 326
Qy	797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTCCTGGCTG 856
Db	325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTCCTGGCTG 266
Qy	857 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGG 916
Db	265 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGG 206
Qy	917 TCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTTAAGAGGGTGGTCGGGA 976

Db	205	TCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTTAAGAGGGTGGCGGA.	146
Qy	977	TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTCACCTCTCCACTGGC	1036
Db	145	TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTCACCTCTCCACTGGC	86
Qy	1037	TGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTCAGTGG	1088
Db	85	TGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTCAGTGG	34

RESULT 3

BX433092/c

LOCUS BX433092 899 bp mRNA linear EST 15-MAY-2003
 DEFINITION BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF013YE04 3-PRIME, mRNA sequence.
 ACCESSION BX433092
 VERSION BX433092.1 GI:30779167
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 899)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 151.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
 Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.
 FEATURES Location/Qualifiers
 source 1. .899
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF013YE04"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
 ORIGIN

Query Match

58.2%; Score 659.2; DB 13; Length 899;

Best Local Similarity 94.4%; Pred. No. 1.9e-127;
Matches 693; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

RESULT 4

AY420885
LOCUS AY420885 753 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY420885
VERSION AY420885.1 GI:39776842
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 753)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..753
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>753
/gene="HCRTR1"
/locus_tag="HCM7373"

ORIGIN

Query Match 49.5%; Score 561.4; DB 29; Length 753;
Best Local Similarity 99.8%; Pred. No. 5.3e-107;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	526	ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC	585
Db	1	ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC	60
Qy	586	ACACGGCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC	645
Db	61	ACACGGCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC	120
Qy	646	CACAGTTGCTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT	705
Db	121	CACAGTTGCTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT	180
Qy	706	TTCCAGATATTCCGCAAGCTCTGGGCCAGATCCCCGGCACACCTCAGCACTGGTG	765

Db	181	TTCCAGATATTCCGCAAGCTCTGGGCCGCCAGATCCCCGGCACACCTCAGCACTGGTG	240
Qy	766	CGGAACCTGGAAGCGCCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAG	825
Db	241	CGGAACCTGGAAGCGCCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAG	300
Qy	826	CCCCAGCCCCGGGCCGCCTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAG	885
Db	301	CCCCAGCCCCGGGCCGCCTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAG	360
Qy	886	ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGC	945
Db	361	ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGC	420
Qy	946	GTCCTCAATGTCCTTAAGAGGGTGGTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT	1005
Db	421	GTCCTCAATGTCCTTAAGAGGGTGGTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT	480
Qy	1006	GTCTACGCCTGCTTCACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC	1065
Db	481	GTCTACGCCTGCTTCACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC	540
Qy	1066	ATCATCTACAACCTCCTCAGTGG	1088
Db	541	ATCATCTACAACCTCCTCAGTGG	563

RESULT 5

AK048781

LOCUS AK048781 3470 bp mRNA linear HTC 20-SEP-2003
 DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2, full insert sequence.
 ACCESSION AK048781
 VERSION AK048781.1 GI:26339571
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3470)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.go.jp/>
URL:<http://fantom.gsc.riken.go.jp/>.

FEATURES Location/Qualifiers

source 1. .3470
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230065B06"

/db_xref="MGI:2415851"
 /db_xref="taxon:10090"
 /clone="C230065B06"
 /tissue_type="cerebellum"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="0 day neonate"
CDS
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 match=1380)
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 VTITCLPATLVVDITETWFFGQSLCKVIPYQLTVSVSVLTLSCIALDRWYAICHPL
 MFKSTAKRARN SIVVIWIVSCIIMIPQAIVMECSSMLPGLANKTTLFTVCDEHWGGEV
 YPKMYHICFFLVTYMAPLCLMILAYLQIFRKLCRQIPGTSSVQRKWKQQQPVSQPR
 GSGQQSKARI SAVAEEIKQIRARRKTARMLMVLLVFAICYLPISILNVLKRVFGMFT
 HTEDRET VYAWFTFSHLVYANSAANPIIYNFLSGKFREEFKAAFSCCLGVHHRQGDR
 LARGRTSTESRKSLTTQISNFNDNVSKLSEHVVILTSISTLPAANGAGPLQNWLQOQGP
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polyA_site
 3470
 /note="putative"

ORIGIN

Query Match 46.8%; Score 530.4; DB 11; Length 3470;
 Best Local Similarity 71.1%; Pred. No. 3.3e-100;
 Matches 718; Conservative 0; Mismatches 286; Indels 6; Gaps 1;

Qy	80	ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT	139
Db	178	ACGACGAGGAATT CCTGC CGGTACCTGTGGAGGGAAACCTACACCCGAAAGAACATGAGT	237
Qy	140	GGGT CCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGCAACACGCTGG	199
Db	238	GGGT CCTGATCGCAGGGTATATCATCGT GTGTTGTGGCTCTCATCGGGAACGT CCTGG	297
Qy	200	TCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	298	TCTGTGTGGCAGTGTGGAAAGAACCAACCATGAGGACAGTCACCAACTACTCATAGTCA	357
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGCCAGCCTGCTGGTGG	319
Db	358	ACCTTTCCCTAGCAGATGTGCTTGACCATCACCTGCCCTCCAGCTACCCCTCGTTGTTG	417
Qy	320	ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGT CATCCCCTATCTACAGG	379
Db	418	ACATCACTGAGACTTGGTCTTGGACAGTCCCTCTGTAAGGT CATT CCTT ATTACAGA	477
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCA TGCCCTGGACCGCTGGTATG	439
Db	478	CTGTGTCA GTGTCTGTTCTACGTTGAGCTGCATTGCCCTGGACCGATGGTACG	537

Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCC GGCGGGCCGTGGCTCCATCCTGG	499
Db	538.	CCATTTGTCAACCCTTGATGTTCAAGAGCACAGCAAACGGGCTCGAAACAGCATCGTG	597
Qy	500	GCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAAGGCTGCAGTCATGGAATGCAGCA	559
Db	598	TCATCTGGATCGTCTCCTGCATCATAATGATTCTCAAGCCATTGTCATGGAGTGCAGCA	657
Qy	560	GTGTGCTGCCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCGTGATGAACGCTGGG	619
Db	658	GCATGCTCCCTGGCCTAGCCAATAAGACCACCCCTCTTACAGTATGTGATGAACACTGGG	717
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	718	GCGGTGAAGTTACCAAAGATGTACCATATCTGCTTCTGGTGACATACATGGCAC	777
Qy	680	CACTGGGCCTCATGGCATGGCTATTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA	739
Db	778	CTCTGTGTTATGATATTGGCTTATCTCAAATATTCCGTAAACTCTGGTGCCGACAGA	837
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCAGAACCTGGAAAGCGCCCTCAGACCAGCTGGGGG	799
Db	838	TTCCCGGAACCTCTTCTGTGGTCAGAGAAAATGGAAGCAGC-----AGCAGCCGGTTT	891
Qy	800	ACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTTCTGGCTGAAG	859
Db	892	CTCAGCCCCGGGGTCCGGACAGCAGAGCAAGGCTGGATTAGCGCTGTTGCTGCTGAGA	951
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT	919
Db	952	TAAAGCAGATCCGAGCACGAAGGAAACAGCCGGATGCTCATGGTTGACTTCTGGTCT	1011
Qy	920	TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTTAAGAGGGTTCGGATGT	979
Db	1012	TTGCAATTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTGGGATGT	1071
Qy	980	TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTCACCTTCTCCCACGGCTGG	1039
Db	1072	TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTCACTTTCTCATGGCTTG	1131
Qy	1040	TGTACGCCAACAGCGTGCCAACCCCATCATCTACAACCTCCTCAGTGG	1089
Db	1132	TATATGCCAACAGTGCTGCAAACCCAATTATTATAATTCTTAGTGG	1181

RESULT 6

AK038551

LOCUS AK038551 3729 bp mRNA linear HTC 19-SEP-2003
 DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230036M08 product:OREXIN RECEPTOR TYPE 2, full insert sequence.
 ACCESSION AK038551
 VERSION AK038551.1 GI:26332642
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3729)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

REFERENCE
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Db	239	GGGT CCTGAT CGCAGGGT ATATCATCGT GTCG TGGCTCTCATCGGG AACGT CCTGG 298
Qy	200	TCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTCATGTCA 259
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Qy	260	ACCTGTCCTGGCTGACGTTCTGGTACTGCTATCTGCCCTGCCGCCAGCCTGCTGGGG 319
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Qy	320	ACATCACTGAGTCCTGGCTGTTGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGG 379
Db	419	ACATCACTGAGACTGGTCTTGACAGTCCTCTGTAAGGTATTCCATTACAGA 478
Qy	380	CTGTGTCGGTGTCAAGTGGCAGTGCTAACTCTCAGCTTACGCCCTGGACCGCTGGTATG 439
Db	479	CTGTGTCAGTGTCTGTGCTGTTACGTTGAGCTGCATTGCCCTGGACCGATGGTACG 538
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGGGCCCGTGGCTCCATCCTGG 499
Db	539	CCATTGTCACCCTTGATGTTCAAGAGCACAGCAAACGGGCTCGAAACAGCATCGTTG 598
Qy	500	GCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCTGCAAGTCATGGAATGCAGCA 559
Db	599	TCATCTGGATCGTCTCCTGCATCATAATGATTCCCAAGCCATTGTCATGGAGTGCAGCA 658
Qy	560	GTGTGCTGCCCTGAGCTAGCCAACCGCACACGGCTCTTCAGTCAGTGTGATGAAACGCTGGG 619
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Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC 679
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Qy	680	CACTGGGCCTCATGCCATGCCATTTCAGATATTCCGAAGCTCTGGGCCAGA 739
Db	779	CTCTGTGCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCACAGA 838
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCAGAACCTGGAGACGCGCCCTCAGACCAGCTGGGGGG 799
Db	839	TTCCCCGGAACTTCTCTGTGGTCAGAGAAAATGGAAGCAGC-----AGCAGCCGGTTT 892
Qy	800	ACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTCCTGGCTGAAG 859
Db	893	CTCAGCCCCGGGGTCCGGACAGCAGAGCAAGGCTGGATTAGCCTGTTGCTGCTGAGA 952
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCT 919
Db	953	TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGACTTCTGGTCT 1012
Qy	920	TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTTAAGAGGGTGTGGATGTT 979
Db	1013	TTGCAATTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTGGGATGT 1072
Qy	980	TCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTCACCTTCTCCACTGGCTGG 1039
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Qy 1040 TGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTCAGTGGA 1089
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Db 1133 TATATGCCAACAGTGCCTGCAAACCCAATTATTTATAATTCTTAGTGGA 1182

RESULT 7

BC035858

LOCUS BC035858 1790 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone IMAGE:5767576, mRNA.
ACCESSION BC035858
VERSION BC035858.1 GI:23959160
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1790)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 79 Row: p Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6006037

This clone has the following problem: retained intron.

FEATURES Location/Qualifiers
source 1. .1790
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5767576"

/tissue_type="Brain, fetal, whole pooled"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 45.9%; Score 519.8; DB 11; Length 1790;
Best Local Similarity 70.5%; Pred. No. 4e-98;
Matches 711; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

Qy 80 ATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTGTACCCAAAACAGTATGAGT 139
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Db 146 ACGACGAGGAATTCCCTGCGGTACCTGTGGAGGAAATACCTGCACCCGAAAGAATATGAGT 205

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db 206 GGGTCCTGATCGCCGGGTACATCATCGTGTGTCGTGGCTCTCATTGGAACGTCCTGG 265

Qy 200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAAACACTTCATTGTCA 259
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Db 266 TTTGTGTGGCAGTGTGGAAGAACACCACATGAGGACGGTAACCAAACACTTCATAGTCA 325

Qy 260 ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db 326 ATCTTTCTGGCTGATGTGCTCGTACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 385

Qy 320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTACATCCCCTATCTACAGG 379
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 386 ATATCACTGAGACCTGGTTTTGGACAGTCCCTTGCAAAAGTATTCCCTATCTACAGA 445

Qy 380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCCTGGTATG 439
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Db 446 CCGTGTCCGTGTCAGTGGCTGTCACACTGAGCTGATCGCCTTGGATCGGTGGTATG 505

Qy 440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGGCCGTGGCTCCATCCTGG 499
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Db 506 CAATCTGTCAACCTTGATGTTAAGAGCACAGCAAAGCAGGGCCGTAACAGCATTGTCA 565

Qy 500 GCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db 566 TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA 625

Qy 560 GTGTGCTGCCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCGTGATGAACGCTGGG 619
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Db 626 CCGTGTCCAGGCTTAGCCAATAAACACCACCCCTTTACGGTGTGATGAGCGCTGGG 685

Qy 620 CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC 679
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Db 686 GTGGTGAAATTATCCAAGATGTACCATCTGTTCTTCTGGTGACATACATGGCAC 745

Qy 680 CACTGGCCTCATGCCATGCCATTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Db 746 CACTGTGCTCATGGTGTGGCTATCTGCAAATATTGCAAACTCTGGTGTGACAGA 805

Qy 740 TCCCCGGCACACCTCAGCACTGGTGCAGAACCTGGAAAGCGCCCTCAGACCAGCTGGGG 799
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Db 806 TCCCTGGAACATCATCTGTTAGTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT 859

Qy	800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCCTTCCTGGCTGAAG	859
Db	860 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGATGAGCGCTGTGGCGCTGAAA	919
Qy	860 TGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCT	919
Db	920 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGATGTTGATGGTTGTGCTTTGGTAT	979
Qy	920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT	979
Db	980 TTGCAATTGCTATCTACCAATTAGCATCCTCAATGTCCTAAAGAGAGTATTGGGATGT	1039
Qy	980 TCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCTGCTCACCTCTCCACTGGCTGG	1039
Db	1040 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTACCTTTCACACTGGCTTG	1099
Qy	1040 TGTACGCCAACAGCGTGCCAACCCCCTACATCTACAACCTCCTCAGTGG	1088
Db	1100 TATATGCCAATAGTGCTGCGAATCCAATTATTATAATTTCAGTGG	1148

RESULT 8

AK079572

LOCUS AK079572 3153 bp mRNA linear HTC 19-SEP-2003
 DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2, full insert sequence.
 ACCESSION AK079572
 VERSION AK079572.1 GI:26348079
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3153)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:<http://genome.gsc.riken.go.jp/>
 URL:<http://fantom.gsc.riken.go.jp/>.
 FEATURES Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="A230091E19"
 /sex="male"
 /tissue_type="hypothalamus"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"

CDS ..
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108..1202
/note="unnamed protein product; OREXIN RECEPTOR TYPE 2
(SWISSPROT|P56719, evidence: FASTY, 98.5%ID, 100%length,
match=1380)
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/codon_start=1
/protein_id="BAC37688.1"
/db_xref="GI:26348080"
/translation="MSSTKLEDSLRRNWSSASELNETQEFPFLNPTDYDDEEFLRYLW
REYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWKNHHMRTVTNYFIVNLSADVL
VTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRWYAICHPL
MFKSTAKRARNISIVVIWVSCIIMIPQAIVMECSSMLPGLANKTTLFTVCDEHWGGEV
YPKMYHICFFLVTYMAPLFLMIAYLQIFRKWLRCRQIPGTSSVVQRKWQQQPVSQPR
GSGQQSKARVSAVAEEIKQIRARRKTARMLMVLLVFAICYLPISILNVLKRVFGMFT
HTEDRETVYAWFTFPHWLVYANSCCKPNYL"

ORIGIN

Query Match 45.8%; Score 519.4; DB 11; Length 3153;
Best Local Similarity 71.0%; Pred. No. 6.3e-98;
Matches 718; Conservative 0; Mismatches 286; Indels 7; Gaps 2;

Qy	80	ATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTGTACCCAAAACAGTATGAGT	139
Db	211	ACGACGAGGAATT CCTGC CGGTACCT GTGGAGGGAAATACCTACACCCGAAAGAATATGAGT	270
Qy	140	GGGT CCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGCCCTGGTGGCAACACGCTGG	199
Db	271	GGGT CCTGATCGCAGGGTATATCATCGTGTGTTCGTGGCTCTCATCGGGAACGTCCTGG	330
Qy	200	TCTGCCTGCCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	331	TCTGTGTGGCAGTGTTGGAAGAACCAACCATGAGGACAGTCACCAACTACTTCATAGTCA	390
Qy	260	ACCTGTC CCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGCCAGCCTGCTGGTGG	319
Db	391	ACCTTCCCTAGCAGATGTGCTTGACCATCACCTGCCTCCAGCTACCCCTCGTTGTTG	450
Qy	320	ACATCACTGAGT CCTGGCTGTT CGGCCATGCCCTCTGCAAGGT CATCCCTATCTACAGG	379
Db	451	ACATCACTGAGACTGGTTCTTGACAGTCCCTCTGTAAGGT CATT CCTATTACAGA	510
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTACATGCCCTGGACCGCTGGTATG	439
Db	511	CTGTGTCA GTGCTGTCTGTTACGTTGAGCTGCATTGCCCTGGACCGATGGTAGC	570
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGGCCGGCGGGCCCGTGGCTCCATCCTGG	499
Db	571	CCATTGTCACCCATTGATGTTCAAGAGCACAGCCAACGGCTCGAAACAGCATCGTTG	630
Qy	500	GCATCTGGCTGTGCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	631	TCATCTGGATCGTCTCCTGCATCATAATGATT CCTCAAGCCATTGTCATGGAGTGCAGCA	690
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGG	619
Db	691	GCATGCTCCCTGCCCTAGCCAATAAGACCAACCCCTTTACAGTATGTGATGAACACTGGG	750

Qy	620 CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	751 GCGGTGAAGTTACCCAAAGATGTACCATATCTGCTTCTTCTGGTGACATACATGGCAC	810
Qy	680 CACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGCAAGCTCTGGGCCGCCAGA	739
Db	811 CTCTGTTCTTATGATATTGGCTTATCTCAAATATTCCGTAAACTCTGGTGCACAGA	870
Qy	740 TCCCCGGCACCACCTCAGCACTGGTGCAGGAACCTGGAAGCGCCCTCAGACCAGCTGGGG	799
Db	871 TTCCCGGAACCTCTCTGTGGTCAGAGAAAATGGAAGCAGC-----AGCAGCCGGTTT	924
Qy	800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCCTCCTGGCTGAAG	859
Db	925 CTCAGCCCCGGGGTCCGGACAGCAGAGCAAGGCTGGTTAGCGCTGTTGCTGCTGAGA	984
Qy	860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT	919
Db	985 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCGGATGCTCATGGTTGACTTCTGGTCT	1044
Qy	920 TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTTAAGAGGGTGTTCGGGATGT	979
Db	1045 TTGCAATTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTGGGATGT	1104
Qy	980 TCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTCACCTCTCCACTGGCTGG	1039
Db	1105 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTCACTTTCCCTATTGGCTTG	1164
Qy	1040 TGTACGCCAACAGC-GCTGCCAACCCATCATCTACAACCTCCTCAGTGG	1089
Db	1165 TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTCTTAGTGGA	1215

RESULT 9

CF147830/c

LOCUS CF147830 790 bp mRNA linear EST 25-JUL-2003
 DEFINITION AGENCOURT_14740202 NIH_MGC_145 Homo sapiens cDNA clone
 IMAGE:6971889 5', mRNA sequence.
 ACCESSION CF147830
 VERSION CF147830.1 GI:33244098
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 790)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: GPCR Consortium
 cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBI02 row: a column: 08
 High quality sequence start: 7
 High quality sequence stop: 738.

FEATURES	Location/Qualifiers
source	1. .790 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6971889" /tissue_type="mixed" /lab_host="DH10B" /clone_lib="NIH_MGC_145" /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match	44.5%	Score	504.4	DB	14	Length	790		
Best Local Similarity	99.8%	Pred. No.	4.7e-95						
Matches	505	Conservative	0	Mismatches	1	Indels	0	Gaps	0

Qy	583 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC	642
Db	790 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC	731
Qy	643 TACCACAGTTGCTTCTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGCCATGGCC	702
Db	730 TACCACAGTTGCTTCTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGCCATGGCC	671
Qy	703 TATTTCAGATATTCCGCAAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTG	762
Db	670 TATTTCAGATATTCCGCAAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTG	611
Qy	763 GTGCGGAACTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGG	822
Db	610 GTGCGGAACTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGG	551
Qy	823 GAGCCCCAGCCCCGGGCCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG	882
Db	550 GAGCCCCAGCCCCGGGCCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG	491
Qy	883 AAGACAGCCAAGATGCTGATGGTGGTGCTGGCTACCTGCCATC	942
Db	490 AAGACAGCCAAGATGCTGATGGTGGTGCTGGCTTCGCCCTGCTACCTGCCATC	431
Qy	943 AGCGTCCTCAATGTCTTAAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAA	1002

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Db      ||||||| 430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371
Qy      1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
Db      ||||||| 370 GCTGTCTACGCCTGCTTCACCTTCTCCCACGGCTGGTGTACGCCAACAGCGCTGCCAAC 311
Qy      1063 CCCATCATCTACAACCTCCTCAGTGG 1088
Db      ||||||| 310 CCCATCATCTACAACCTCCTCAGTGG 285

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RESULT 10

AY420886

LOCUS AY420886 750 bp DNA linear GSS 17-DEC-2003
 DEFINITION Pan troglodytes HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY420886
 VERSION AY420886.1 GI:39776843
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 750)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 750)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them
 based on alignment.
 FEATURES Location/Qualifiers
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 . . . /organism="Pan troglodytes"
 . . . /mol_type="genomic DNA"
 . . . /db_xref="taxon:9598"
 gene <1. .>750
 . . . /gene="HCRTR1"
 . . . /locus_tag="HCM7373"

ORIGIN

Query Match 41.9%; Score 474.2; DB 29; Length 750;
 Best Local Similarity 84.5%; Pred. No. 9.7e-89;
 Matches 476; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

RESULT 11

AL535838

LOCUS AL535838 1001 bp mRNA linear EST 12-MAY-2003
DEFINITION AL535838 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF013YE04 5-PRIME, mRNA sequence.
ACCESSION AL535838
VERSION AL535838.2 GI:30542758
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1001)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12799331.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 151.r For
 more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r>. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.

FEATURES Location/Qualifiers

source 1. .1001
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF013YE04"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match	41.7%	Score	472	DB	9	Length	1001		
Best Local Similarity	92.0%	Pred. No.	3.2e-88						
Matches	544	Conservative	13	Mismatches	25	Indels	9	Gaps	6

Qy 377 AGGCTGTGTCCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGT 436
 |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
 Db 415 AGGCTGTGTCCCGTGTCAAGTGGCAGTGCTAACTCTMANCTTCATGCMCTGGACCGCTGGT 474

Qy 437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGCGGGCCGTGGCTCCATCC 496
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 Db 475 ATGCHATCTGCYACCCACTATTGTTCAAGARCACAGCCCAGGCGGGCCGTGGCTCCATCC 534

Qy 497 TGGGCATCTGGGCTGTGTCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCA 556
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 Db 535 TNNGNATCTGGCTNTTCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCA 594

Qy 557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCAGTCTGATGATGAACGCT 616
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 595 GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTTCTCAGTCTGATGATGAACGCT 654

Qy 617 GGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGG 676
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 Db 655 GGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGG 714

Qy 677 CCCCCACTGGGCTCATGGCCATGGCCTATTCCAGATATTCCGCAAGCTGGGGCCGCC 736
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 Db 715 CCCCCACTGGGCTCATGGCCATGGCCTATTCCAGATATTCCGCAAGCTGGGGCCGCC 774

RESULT 12

AY420887

LOCUS AY420887 726 bp DNA linear GSS 17-DEC-2003
 DEFINITION Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY420887
 VERSION AY420887.1 GI:39776844
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 726)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 726)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
 source 1..726
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene <1..>726
 /gene="HCRTR1"
 /locus_tag="HCM7373"
 ORIGIN

Query Match 41.4%; Score 468.6; DB 29; Length 726;
 Best Local Similarity 89.5%; Pred. No. 1.4e-87;
 Matches 504; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy	526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC	585
Db	1 ATGGTGCCCCAGGCTGCTGTCAATGGAGTGCAGCAGCAGTGCCTGAGCTAGCCAATCGC	60
Qy	586 ACACGGCTTCTCAGTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAAGATCTAC	645
Db	61 ACCCGGCTTCTCTGTCTGTGATGAGCAGTGGCAGATGAACCTACCCAAAGATCTAT	120
Qy	646 CACAGTTGCTTCTTATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTAT	705
Db	121 CACAGCTGCTTTTCATTGTCACCTACCTGGCCCCACTGGCCTCATGGCTATGGCTAT	180
Qy	706 TTCCAGATATTCCGCAAGCTCTGGGCCGCCAGATCCCCGGCACACCCTCAGCACTGGTG	765
Db	181 TTCCAGATTTCCGCAAGCTCTGGGCCGCCAGATCCCTGGTACCACTCAGCCTTGGTG	240
Qy	766 CGGAACTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAG	825
Db	241 CGGAACTGGAAACGGCCCTCGGAACAATGGAGGCTCAGCACCAAGGGCTCTGTACAGAG	300
Qy	826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGGTGCACGGAGGAAG	885
Db	301 CCCCAGCCCCGGGGCCGAGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG	360
Qy	886 ACAGCCAAGATGCTGATGGTAGTGGTAGTCCTGGTACCTCTGGTATCTGCCATCAGC	945
Db	361 ACGGCTAACATGCTGATGGTAGTCCTGGTACCTCTGGTACCTCTGGTATCTGCCATCAGT	420
Qy	946 GTCTCAATGCTTAAGAGGGTGGTCGGGATGTTCCGCCAGCAGTGCACCGCGAAGCT	1005
Db	421 GTCTCAATGCTTAAGAGAGTGGTAGTCGGGATGTTCCGCCAGCAGCAGCGACCGGAAGCC	480
Qy	1006 GTCTACGCCCTGCTTCACCTCTCCACTGGCTGGTACGCCAACAGCGCTGCCAACCCC	1065
Db	481 GTCTACGCCCTGCTTCACCTCTCCACTGGCTAGTGTACGCCAACAGTGCACGCCAACCT	540
Qy	1066 ATCATCTACAACCTCCTCAGTGG 1088	
Db	541 ATCATCTACAACCTCCTCAGTGG 563	

272

135

RESULT 13

BM926746

LOCUS BM926746 993 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6681991 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767576
 5', mRNA sequence.
 ACCESSION BM926746
 VERSION BM926746.1 GI:19377125
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12826 row: a column: 17
 High quality sequence stop: 684.

FEATURES Location/Qualifiers
source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5767576"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 34.7%; Score 393.2; DB 12; Length 993;
 Best Local Similarity 72.1%; Pred. No. 1e-71;
 Matches 512; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

Qy	80 ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT	139
Db	145 ACGACGAGGAATT CCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT	204
Qy	140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTCGGCCCTGGTGGCAACACGCTGG	199
Db	205 GGGTCCTGATGCCGGGTACATCATCGTGGCTCTCATTGGAACGTCTGG	264
Qy	200 TCTGCCTGCCGTGTGGCGGAACCACCATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	265 TTTGTGTGGCAGTGTGGAAGAACCAACATGAGGACGGTAACCAACTACTTCATAGTCA	324
Qy	260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	325 ATCTTTCTGGCTGATGTGCTCGTGACCATCACCTGCCCTCAGCCACACTGGTCGTGG	384
Qy	320 ACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCACAGG	379

Db	385	ATATCACTGAGACCTGGTTTTGGACAGTCCCTTGCAAAGTGATTCCCTATCTACAGA	444
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCCTGGTATG	439
Db	445	CCGTGTGGTGTCTGTCTGCCTCACACTGAGCTGATGCCCTGGATCGGTGGTATG	504
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCAGGGCCGTGGCTCCATCCTGG	499
Db	505	CAATCTGTCAACCTTGTGATGTTAACAGACAGCAAAGCAGGGCCGTAACAGCATTGTCA	564
Qy	500	GCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	565	TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA	624
Qy	560	GTTGCTGCCCTGAGCTAGCCAACCGCACACGGCTCTTCAGTCTGTGATGAACGCTGGG	619
Db	625	CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCCTCTTACGGTGTGATGAGCGCTGGG	684
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	685	GTGGTGAATTTATCCAAGATGTACACATCTGTTCTTCTGGTACATACATGGCAC	744
Qy	680	CACTGGGCCTCATGCCATGCCATTTCAGATATTCCGCAAGCTCTGGGCCGCCAGA	739
Db	745	CACTGTGTCATGGTGTGGCTTATCTGCAAATATTTCGCAAACCTCTGGTGTGACAGA	804
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCAGAACCTGGAAAGCGCCCTCAGAC	789
Db	805	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAAGCCCTGGAGCC	854

RESULT 14

BX119589

LOCUS BX119589 543 bp mRNA linear EST 10-FEB-2003
 DEFINITION BX119589 Soares infant brain 1NIB Homo sapiens cDNA clone
 IMAGP998P20171 ; IMAGE:40608, mRNA sequence.
 ACCESSION BX119589
 VERSION BX119589.1 GI:28289997
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.
 TITLE Human UnigeneSet - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGP998P20171.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human UnigeneSet - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
Location/Qualifiers

ORIGIN

Query Match 33.1%; Score 374.6; DB 13; Length 543;
Best Local Similarity 98.7%; Pred. No. 6e-68;
Matches 377; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG 120

Ov 121 TACCCAAAACAGTATGAGTGAGTCCTCATCGCAGCTATGTGGCTGTGTTCGTCGTGGCC 180

Db 278 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 337

Db 338 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACCCACATGAGGACAGTC 397

QY 301 CCGGCCAGCCTGCTGGACATCACTGAGTCCTGGCTGTCGGCCATGCCCTCTGCAAG 360

458 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTCGGCCATGCCCTGTGAAAG 517

RESULT 15
CF147829

LOCUS CF147829 788 bp mRNA linear EST 25-JUL-2003
 DEFINITION AGENCOURT_14740210 NIH_MGC_145 Homo sapiens cDNA clone
 IMAGE:6971890 5', mRNA sequence.
 ACCESSION CF147829
 VERSION CF147829.1 GI:33244097
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 788)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: GPCR Consortium
 cDNA Library Preparation: GPCR Consortium
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBI02 row: a column: 09
 High quality sequence start: 9
 High quality sequence stop: 772.
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971890"
 /tissue_type="mixed"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_145"
 /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
 varies by clone; ORFs were PCR-amplified and cloned into
 pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
 clone and include the following: 5'-EcoRV-XmnI/XbaI-3',
 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
 For information about which gene each clones represents,
 please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBI.preSV.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 32.4%; Score 367; DB 14; Length 788;

Best Local Similarity 72.7%; Pred. No. 2.8e-66;
Matches 472; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy	80	ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGTATTATCTGTACCCAAAACAGTATGAGT 139
Db	140	ACGACGAGGAATTCTGCCTGCGGTACCTGTGGAGGGAAATACCTGCACCCGAAAGAATATGAGT 199
Qy	140	GGGTCCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGCAACACGCTGG 199
Db	200	GGGTCCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAAACGTCTGG 259
Qy	200	TCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
Db	260	TTTGTGTGGCAGTGTGGAAGAACCAACCATGAGGACGGTAACCAACTACTTCATAGTCA 319
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
Db	320	ATCTTTCTCTGGCTGATGTGCTCGTACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 379
Qy	320	ACATCACTGAGTCCTGGCTGTCGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGG 379
Db	380	ATATCACCGAGACCTGGTTTTGGACAGTCCCTTGCAAAGTGATTCTTATCTACAGA 439
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGTATG 439
Db	440	CCGTGTGGTGTCTGTCTGCCTCACACTGAGCTGTATGCCCTGGATCGGTGGTATG 499
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGGGCCGTGGCTCCATCCTGG 499
Db	500	CAATCTGTCACCCTTGATGTTAACAGACAGCAAAGCGGGCCGTAAACAGCATTGTCA 559
Qy	500	GCATCTGGCTGTGCGCTGGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA 559
Db	560	TCATCTGGATTGTCTCCTGCATTATAATGATTCTCAGGCCATCGTCATGGAGTGCAGCA 619
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGG 619
Db	620	CTGTGTTCCCAGGCTTAGCCAATAAAACCACCCCTTTACGGTGTGTGATGAGCGCTGGG 679
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC 679
Db	680	GTGGTGAATTTATCCAAGATGTACCACATCTGTTCTTCTGGTACATACATGGCAC 739
Qy	680	CACTGGGCCTCATGCCATGGCTATTCCAGATATTCCGCAAGCTCTG 728
Db	740	CACTGTGTCTCATGGTGTGGCTATCTGNCAATACTCGCANACTCTG 788

Search completed: October 15, 2004, 22:50:33
Job time : 3299.03 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 4590.56 Seconds
(without alignments)
10697.520 Million cell updates/sec

Title: US-10-070-532-5

Perfect score: 1133

Sequence: 1 atggagccctcagccacccc.....tcctgaccatcggtccccgg 1133

Scoring table: IDENTITY_NUC

Gapop 10.0., Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

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5: gb_ov:*

6: gb_pat:*

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13: gb_un:*

14: gb_vi:*

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19: em_mu:*

20: em_om:*

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22: em_ov:*

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28: em_un:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
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34: em_htg_pln:*
35: em_htg_rod:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1131.4	99.9	1133	6	E43973	E43973 Novel G pro
2	1131.4	99.9	1133	6	AX746120	AX746120 Sequence
3	1131.4	99.9	1133	6	BD185454	BD185454 Human neu
4	1128.2	99.6	1170	6	E43972	E43972 Novel G pro
5	1128.2	99.6	1170	6	AX746118	AX746118 Sequence
6	1114.4	98.4	1116	6	AR216119	AR216119 Sequence
7	1086.4	95.9	1209	6	AR216117	AR216117 Sequence
8	1086.4	95.9	1564	6	E43974	E43974 Novel G pro
9	1086.4	95.9	1564	6	E50810	E50810 Novel G pro
10	1086.4	95.9	1564	6	E50811	E50811 Novel G pro
11	1086.4	95.9	1564	6	AX299473	AX299473 Sequence
12	1086.4	95.9	1564	6	AX299475	AX299475 Sequence
13	1086.4	95.9	1564	6	AX549082	AX549082 Sequence
14	1086.4	95.9	1564	6	AX746121	AX746121 Sequence
15	1086.4	95.9	1564	6	AX840912	AX840912 Sequence
16	1086.4	95.9	1564	9	AF041243	AF041243 Homo sapi
17	1084.8	95.7	1110	6	AR216118	AR216118 Sequence
18	1081.6	95.5	1209	6	BD185452	BD185452 Human neu
19	1081.6	95.5	1278	6	AX280925	AX280925 Sequence
20	1076.8	95.0	1110	6	BD185453	BD185453 Human neu
21	892.8	78.8	2200	10	AY336083	AY336083 Mus muscu
22	891.2	78.7	2469	10	AF041244	AF041244 Rattus no
23	697.6	61.6	843	6	AR109899	AR109899 Sequence
24	670.6	59.2	789	6	AR109632	AR109632 Sequence
25	670.6	59.2	789	6	E12154	E12154 cDNA encodi
26	670.6	59.2	789	6	AR300942	AR300942 Sequence
27	579.6	51.2	781	10	AF394596	AF394596 Mus muscu
28	554.4	48.9	3114	10	AF041246	AF041246 Rattus no
29	530.4	46.8	1545	10	AY336084	AY336084 Mus muscu
30	530.4	46.8	2117	10	AY336085	AY336085 Mus muscu
31	520.8	46.0	1633	6	E33974	E33974 cDNA clone
32	520.8	46.0	1843	6	AX549084	AX549084 Sequence
33	520.8	46.0	1843	6	AX840914	AX840914 Sequence

34	520.8	46.0	1878	9	AF041245	AF041245 Homo sapi
35	516	45.5	1335	6	AX280927	AX280927 Sequence
36	514.4	45.4	1805	4	AF164626	AF164626 Canis fam
37	496.2	43.8	597	10	AY255599	AY255599 Mus muscu
38	329.2	29.1	382	4	AF499612	AF499612 Ovis arie
39	304.2	26.8	637	10	AF394597	AF394597 Mus muscu
40	281.6	24.9	328	4	AB092488	AB092488 Bos tauru
41	263.2	23.2	501	4	AF532967	AF532967 Ovis arie
42	249.2	22.0	344	9	F202078S03	AF202080 Homo sapi
43	249.2	22.0	9785	6	AR178605	AR178605 Sequence
44	249.2	22.0	9785	6	AX088174	AX088174 Sequence
45	249.2	22.0	9785	9	AY062030	AY062030 Homo sapi

ALIGNMENTS

RESULT 1

E43973

LOCUS E43973 1133 bp DNA linear PAT 31-JAN-2002
 DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
 ACCESSION E43973
 VERSION E43973.1 GI:18625172
 KEYWORDS JP 2000106888-A/2.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1133)
 AUTHORS Bergsma,D.J. and Ellis,C.E.
 TITLE Novel G protein-coupled receptor (HFGAN72Y)
 JOURNAL Patent: JP 2000106888-A 2 18-APR-2000;
 SMITHKLINE BEECHAM CORP
 COMMENT OS Unidentified
 PN JP 2000106888-A/2
 PD 18-APR-2000
 PF 21-JUL-1999 JP 1999206116
 PR 30-APR-1997 US 08/846705
 PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS
 PC C12N15/09, A61K38/00, A61K38/00, A61K45/00, A61K48/00, A61P1/00, PC
 A61P1/14,
 PC A61P9/02, A61P9/04, A61P9/10, A61P9/12, A61P11/06, A61P13/02, PC
 A61P13/08,
 PC A61P19/10, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,
 PC A61P31/04,
 PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P37/08,
 PC A61P43/00,
 PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, G01N33/566,
 PC G01N33/577//
 PC C12P21/08, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,
 PC A61K37/02,
 PC A61K37/02, C12N5/00, (C12N15/00, C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..1133
 FT /organism='Unidentified'.
 FEATURES Location/Qualifiers

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ORIGIN

Query Match      99.9%;  Score 1131.4;  DB 6;  Length 1133;
Best Local Similarity 99.9%;  Pred. No. 2.2e-218;
Matches 1132;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGTATTCTG 120
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGTATTCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCTCGTGGCC 180
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCTCGTGGCC 180

Qy      181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCC 300
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Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCC 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGG 480
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Qy      481 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
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Db      601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy      661 ATTGTACACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
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Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC 780
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 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC 780
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 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
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 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||||
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG 900
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG 900
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 Qy 901 ATGGTGGTGCCTGGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGCCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
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 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
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 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
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 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Qy 1081 CTCAGTGGATGTAAGAGAAGAGCTAGTTCTGCTGACCATCGTCCCCGG 1133
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 Db 1081 CTCAGTGGATGTAAGAGAAGAGCTAGTTCTGCTGACCATCGTCCCCGG 1133

RESULT 2

AX746120

LOCUS AX746120 1133 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 3 from Patent EP1156110.
 ACCESSION AX746120
 VERSION AX746120.1 GI:31744926
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bergsma, D.J. and Ellis, C.E.
 TITLE G-protein coupled receptor (HFGAN72Y)
 JOURNAL Patent: EP 1156110-A 3 21-NOV-2001;
 SMITHKLINE BEECHAM CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..1133
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="HGS EST 557082"

ORIGIN

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;
 Best Local Similarity 99.9%; Pred. No. 2.2e-218;
 Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG	120
Db	61	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCTCGTGGCC	180
Qy	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	480
Qy	481	GCCCCGTGGCTCCATCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCCAGGCT	540
Db	481	GCCCCGTGGCTCCATCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGCCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATCGTGACGGAGGAAGACAGCCAAGATGCTG 900
 |||||||
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATCGTGACGGAGGAAGACAGCCAAGATGCTG 900
 |||||||
 Qy 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
 |||||||
 Db 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
 |||||||
 Qy 961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
 |||||||
 Db 961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
 |||||||
 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 3

BD185454

LOCUS BD185454 1133 bp DNA linear PAT 17-JUN-2003
DEFINITION Human neuropeptide receptor.
ACCESSION BD185454
VERSION BD185454.1 GI:31877654
KEYWORDS JP 2002360288-A/3.
SOURCE unidentified
ORGANISM unidentified
 unclassified.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Soppet, D.R., Li, Y. and Rosen, C.A.
TITLE Human neuropeptide receptor
JOURNAL Patent: JP 2002360288-A 3 17-DEC-2002;
 HUMAN GENOME SCIENCES INC
COMMENT
 OS Unidentified
 PN JP 2002360288-A/3
 PD 17-DEC-2002
 PF 02-MAY-2002 JP 2002130838
 PI DANIEL R SOPPET, YI LI, CRAIG A ROSEN
 PC C12N15/09, A61K31/7088, A61K38/00, A61K45/00, A61K48/00, A61P3/04,
 PC A61P3/06,
 PC A61P3/10, A61P9/10, A61P9/12, A61P25/08, A61P25/18, A61P25/22, PC
 A61P25/28,
 PC A61P35/00, A61P43/00, C07K14/705, C07K16/24, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12Q1/68, C12N15/00, C12N5/00, A61K37/02 CC
 Strandedness: Single;
 CC Topology: Linear;
 CC Human neuropeptide receptor
FH Key Location/Qualifiers
FT source 1..1133
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1..1133
 /organism="unidentified"

/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;
Best Local Similarity 99.9%; Pred. No. 2.2e-218;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120

Qy 121 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCGTGGCC 180
Db 121 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360
Db 301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCCTATCTACAGGCTGTGTCGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480

Qy 481 GCCCGTGGCTCCATCTGGCATTGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCTGGCATTGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
Db 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC 780

Db	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC 780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy	901	ATGGTGGTGTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
Db	901	ATGGTGGTGTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Db	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
Qy	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
Db	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 4

E43972

LOCUS E43972 1170 bp DNA linear PAT 31-JAN-2002
 DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
 ACCESSION E43972
 VERSION E43972.1 GI:18625171
 KEYWORDS JP 2000106888-A/1.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1170)
 AUTHORS Bergsma, D.J. and Ellis, C.E.
 TITLE Novel G protein-coupled receptor (HFGAN72Y)
 JOURNAL Patent: JP 2000106888-A 1 18-APR-2000;
 SMITHKLINE BEECHAM CORP
 COMMENT OS Unidentified
 PN JP 2000106888-A/1
 PD 18-APR-2000
 PF 21-JUL-1999 JP 1999206116
 PR 30-APR-1997 US 08/846705
 PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS
 PC C12N15/09, A61K38/00, A61K38/00, A61K45/00, A61K48/00, A61P1/00, PC
 A61P1/14,
 PC A61P9/02, A61P9/04, A61P9/10, A61P9/12, A61P11/06, A61P13/02, PC
 A61P13/08,
 PC A61P19/10, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,
 PC A61P31/04,
 PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P37/08,
 PC A61P43/00,

PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, G01N33/566,
 PC G01N33/577/
 PC C12P21/08, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,
 PC A61K37/02,
 PC A61K37/02, C12N5/00, (C12N15/00, C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..1170
 FT /organism='Unidentified'.
FEATURES
 source Location/Qualifiers
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
ORIGIN
 Query Match 99.6%; Score 1128.2; DB 6; Length 1170;
 Best Local Similarity 99.7%; Pred. No. 9.6e-218;
 Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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 Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60
 |||||||
 Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
 |||||||
 Db 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
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 Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGTCTCGTGGCC 180
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 Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGTCTCGTGGCC 180
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 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
 |||||||
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
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 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
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 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
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 Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG 360
 |||||||
 Db 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG 360
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 Qy 361 GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
 |||||||
 Db 361 GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
 |||||||
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
 |||||||
 Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGCCATCATGGTGCCAGGGCT 540
 |||||||
 Db 481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGCCATCATGGTGCCAGGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTCTCTCA 600
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 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTCTCTCA 600

 Qy 601 GTCTGTGATGAAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660
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 Db 601 GTCTGTGATGAAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660

 Qy 661 ATTGTACACTACCTGGCCCCACTGGCCTCATGCCATGCCATTTCAGATATTCCGC 720
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 Db 661 ATTGTACACTACCTGGCCCCACTGGCCTCATGCCATGCCATTTCAGATATTCCGC 720

 Qy 721 AAGCTCTGGGGCCGAGATCCCCGGCACCAACCTCAGCACTGGTGCAGACTGGAAGCGC 780
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 Db 721 AAGCTCTGGGGCCGAGATCCCCGGCACCAACCTCAGCACTGGTGCAGACTGGAAGCGC 780

 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
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 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840

 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

 Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960

 Qy 961 AAGAGGGTGGTGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC 1020
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 Db 961 AAGAGGGTGGTGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC 1020

 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
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 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080

 Qy 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCCTGACCATCGTGGCCCGG 1133
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 Db 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGCTCTGTCCCTGCCATCGTGGCCCGG 1133

RESULT 5

AX746118

LOCUS AX746118 1170 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 1 from Patent EP1156110.
 ACCESSION AX746118
 VERSION AX746118.1 GI:31744924
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bergsma, D.J. and Ellis, C.E.
 TITLE G-protein coupled receptor (HFGAN72Y)
 JOURNAL Patent: EP 1156110-A 1 21-NOV-2001;
 SMITHKLINE BEECHAM CORPORATION (US)

FEATURES	Location/Qualifiers
source	1. .1170 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
gene	1. .1170 /gene="HFGAN72Y"
CDS	1. .1170 /gene="HFGAN72Y" /codon_start=1 /protein_id="CAD97474.1" /db_xref="GI:31744925" /translation="MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQ YEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA SLLVDITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWAICHPLLFKSTARR ARGSILGIWAVSLAIMVPQAAMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSC FFIVTYLAPLGLMAMAYFQIFRKLGRCIPGTTTSALVRNWKRPSDQLGDLEQGLSGEP OPRGRAGFLAEVKQMRARRKTAKMIVLLVFALCYLPISVNLVLRVFGMFRQASDRE AVYACFTFSHWLVYANSAANPIIYNFLSGCCKEKLALSCPSCPGHDPLAALCS"

ORIGIN

Query Match 99.6%; Score 1128.2; DB 6; Length 1170;
 Best Local Similarity 99.7%; Pred. No. 9.6e-218;
 Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTCTG 120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTCTG 120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Qy	181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACACATGAGGACAGTC 240
Db	181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACACATGAGGACAGTC 240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Qy	301 CGGGCCAGCCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360
Db	301 CGGGCCAGCCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360
Qy	361 GTCATCCCTATCTACAGGCTGTGTCGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420
Db	361 GTCATCCCTATCTACAGGCTGTGTCGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480

Qy 481 GCCCGTGGCTCATCCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 540
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 Db 481 GCCCGTGGCTCATCCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 540

 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
 ..|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600

 Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTTT 660
 ..|||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTTT 660

 Qy 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
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 Db 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

 Qy 721 AAGCTCTGGGCCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCTGGAAGCGC 780
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 Db 721 AAGCTCTGGGCCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCTGGAAGCGC 780

 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
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 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840

 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

 Qy 901 ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT 960

 Qy 961 AAGAGGGTGGATGTTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCGTGCTTC 1020
 ..|||||||||||||||||||||||||||||||||||||||||||
 Db 961 AAGAGGGTGGATGTTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCGTGCTTC 1020

 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 ..|||||||||||||||||||||||||||||||||||||||||||
 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080

 Qy 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTCCCCGG 1133
 ..|||||||||||||||||||||||||||||||||||
 Db 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGCTCTGTCCTGCCATCGTCCCCGG 1133

RESULT 6

AR216119

LOCUS	AR216119	1116 bp	DNA	linear	PAT 25-SEP-2002
DEFINITION	Sequence 5 from patent US 6410701.				
ACCESSION	AR216119				
VERSION	AR216119.1 GI:23314432				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown. Unclassified.				
REFERENCE	1 (bases 1 to 1116)				
AUTHORS	Soppet, D.R., Li, Y. and Rosen, C.A.				

TITLE Human neuropeptide receptor
JOURNAL Patent: US 6410701-A 5 25-JUN-2002;
FEATURES Location/Qualifiers
source 1. .1116
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 98.4%; Score 1114.4; DB 6; Length 1116;
Best Local Similarity 99.9%; Pred. No. 5.9e-215;
Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db |||||||
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db |||||||
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db |||||||
Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db |||||||
Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db |||||||
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db |||||||
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 360
Db |||||||
Qy 361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db |||||||
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGG 480
Db |||||||
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGG 480
Db |||||||
Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 540
Db |||||||
Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db |||||||
Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT 660
Db |||||||
Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
 Qy 721 AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAAGCTGGAAGCGC 780
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 Db 721 AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAAGCTGGAAGCGC 780
 |||||||
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
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 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
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 Qy 841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 |||||||
 Db 841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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 Qy 901 ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
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 Qy 961 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
 |||||||
 Db 961 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
 |||||||
 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
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 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116

RESULT 7

AR216117

LOCUS AR216117 1209 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 1 from patent US 6410701.
 ACCESSION AR216117
 VERSION AR216117.1 GI:23314430
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1209)
 AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.
 TITLE Human neuropeptide receptor
 JOURNAL Patent: US 6410701-A 1 25-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..1209
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1209;
 Best Local Similarity 99.9%; Pred. No. 2.7e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60

Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG	360
Db	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG	360
Qy	361 GTCATCCCCATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361 GTCATCCCCATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601 GTCTGTGATGAAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	601 GTCTGTGATGAAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Qy	661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATAATTCCGC	720
Db	661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATAATTCCGC	720
Qy	721 AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGAAGCGC	780
Db	721 AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGAAGCGC	780
Qy	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT 960
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
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 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
 Qy 1081 CTCAGTGG 1088
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 Db 1081 CTCAGTGG 1088

RESULT 8

E43974

LOCUS E43974 1564 bp DNA linear PAT 31-JAN-2002
 DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
 ACCESSION E43974
 VERSION E43974.1 GI:18625173
 KEYWORDS JP 2000106888-A/3.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1564)
 AUTHORS Bergsma,D.J. and Ellis,C.E.
 TITLE Novel G protein-coupled receptor (HFGAN72Y)
 JOURNAL Patent: JP 2000106888-A 3 18-APR-2000;
 SMITHKLINE BEECHAM CORP
 COMMENT OS Unidentified
 PN JP 2000106888-A/3
 PD 18-APR-2000
 PF 21-JUL-1999 JP 1999206116
 PR 30-APR-1997 US 08/846705
 PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS
 PC C12N15/09, A61K38/00, A61K38/00, A61K45/00, A61K48/00, A61P1/00, PC
 A61P1/14,
 PC A61P9/02, A61P9/04, A61P9/10, A61P9/12, A61P11/06, A61P13/02, PC
 A61P13/08,
 PC A61P19/10, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,
 PC A61P31/04,
 PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P37/08,
 PC A61P43/00,
 PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, G01N33/566,
 PC G01N33/577//
 PC C12P21/08, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,
 PC A61K37/02,
 PC A61K37/02, C12N5/00, (C12N15/00, C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1. .1564

FT /organism='Unidentified'.
 FEATURES Location/Qualifiers
 source 1. .1564
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333
Qy	181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	513
Qy	361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	480
Db	574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	633
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	540
Db	634 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	693
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCAACAGTTGCTTCTTT	660
Db	754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCAACAGTTGCTTCTTT	813
Qy	661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720

Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCATGGCTATTCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGC GGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGC GGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCC TT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCC TT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC TGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC TGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACA ACTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACA ACTTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 9

E50810
LOCUS E50810 1564 bp DNA linear PAT 18-JUN-2001
DEFINITION Novel G protein-bound receptor (HFGAN 72X).
ACCESSION E50810
VERSION E50810.1 GI:13023197
KEYWORDS JP 2000060578-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1564)
AUTHORS Derk, J.B. and Catharine, E.E.
TITLE Novel G protein-bound receptor (HFGAN 72X)
JOURNAL Patent: JP 2000060578-A 1 29-FEB-2000;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 2000060578-A/1
PD 29-FEB-2000
PF 21-JUL-1999 JP 1999206115
PR 30-APR-1997 US 08/846704
PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS
PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,
PC A61K45/00,
PC A61K48/00, A61P3/04, A61P9/00, A61P11/06, A61P13/00, A61P25/00, PC
A61P25/16,

PC A61P25/18, A61P25/20, A61P25/22, A61P31/04, A61P31/10, A61P31/12,
 PC A61P31/18,
 PC A61P35/00, A61P37/00, C07K14/705, C12N5/10, C12P21/02, C12Q1/02, PC
 G01N33/53,
 PC G01N33/566//C07K16/28, C12N15/00, A61K37/02, C12N5/00 CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1. .1564
 FT /organism='Unidentified'.
FEATURES Location/Qualifiers
 source 1. .1564
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	214 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	273
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	333
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	360
Db	454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	513
Qy	361 GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACCTCTCAGCTTCATC	420
Db	514 GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACCTCTCAGCTTCATC	573
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	480
Db	574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	633
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCAGGGCT	540
Db	634 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCAGGGCT	693

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600
 |||||||
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 753
 |||||||
 Qy 601 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
 |||||||
 Db 754 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 813
 |||||||
 Qy 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGCCATGCCATTTCAGATATTCCGC 720
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 Db 814 ATTGTACCTACCTGGCCCCACTGGCCTCATGCCATGCCATTTCAGATATTCCGC 873
 |||||||
 Qy 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGAAGCGC 780
 |||||||
 Db 874 AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGAAGCGC 933
 |||||||
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||||
 Db 934 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 993
 |||||||
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 |||||||
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
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 Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
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 Db 1054 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 1113
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 Qy 961 AAGAGGGTGGATGTCGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC 1020
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 Db 1114 AAGAGGGTGGATGTCGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC 1173
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 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 |||||||
 Db 1174 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1233
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 Qy 1081 CTCAGTGG 1088
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 Db 1234 CTCAGTGG 1241

RESULT 10

E50811

LOCUS E50811 1564 bp DNA linear PAT 18-JUN-2001
 DEFINITION Novel G protein-bound receptor (HFGAN 72X).
 ACCESSION E50811
 VERSION E50811.1 GI:13023198
 KEYWORDS JP 2000060578-A/2.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1564)
 AUTHORS Derk, J.B. and Catharine, E.E.
 TITLE Novel G protein-bound receptor (HFGAN 72X)
 JOURNAL Patent: JP 2000060578-A 2 29-FEB-2000;
 SMITHKLINE BEECHAM CORP
 COMMENT OS Unidentified

PN JP 2000060578-A/2
 PD 29-FEB-2000
 PF 21-JUL-1999 JP 1999206115
 PR 30-APR-1997 US 08/846704
 PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS
 PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,
 PC A61K45/00,
 PC A61K48/00, A61P3/04, A61P9/00, A61P11/06, A61P13/00, A61P25/00, PC
 A61P25/16,
 PC A61P25/18, A61P25/20, A61P25/22, A61P31/04, A61P31/10, A61P31/12,
 PC A61P31/18,
 PC A61P35/00, A61P37/00, C07K14/705, C12N5/10, C12P21/02, C12Q1/02, PC
 G01N33/53,
 PC G01N33/566//C07K16/28, C12N15/00, A61K37/02, C12N5/00 CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1. .1564
 FT /organism='Unidentified'.
FEATURES
 source Location/Qualifiers
 1. .1564
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
ORIGIN
 Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
 Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 214 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 273
 Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
 Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 334 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 393
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
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 Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453
 Qy 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 454 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 513
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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 Db 514 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 633
Qy	481	GCCC GTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 540
Db	634	GCCC GTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA 600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA 753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCTATTCCAGATATTCCGC 720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCTATTCCAGATATTCCGC 873
Qy	721	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGAACTGGAAGCGC 780
Db	874	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGAACTGGAAGCGC 933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
Db	1054	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 1113
Qy	961	AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Db	1114	AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC 1080
Db	1174	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC 1233
Qy	1081	CTCAGTGG 1088
Db	1234	CTCAGTGG 1241

RESULT 11

AX299473

LOCUS	AX299473	1564 bp	DNA	linear	PAT 26-NOV-2001
DEFINITION	Sequence 1 from Patent EP1154019.				
ACCESSION	AX299473				
VERSION	AX299473.1	GI:17129230			
KEYWORDS					

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bergsma,D.J. and Ellis,C.E.
 TITLE G-protein coupled receptor (hfgan72x)
 JOURNAL Patent: EP 1154019-A 1 14-NOV-2001;
 SmithKline Beecham Corporation (US)
 FEATURES Location/Qualifiers
 source 1. .1564
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
        |||||||  

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGAATTATCTG 120
        |||||||  

Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGAATTATCTG 273
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Qy      121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
        |||||||  

Db      274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
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Qy      181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
        |||||||  

Db      334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 393
        |||||||  

Qy      241 ACCAACTACTCATTGTCACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
        |||||||  

Db      394 ACCAACTACTCATTGTCACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453
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Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG 360
        |||||||  

Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG 513
        |||||||  

Qy      361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 420
        |||||||  

Db      514 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 573
        |||||||  

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
        |||||||  

Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 633
        |||||||  

Qy      481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTC 540
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Db      634 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTC 693
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Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
    
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Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 12

AX299475

LOCUS AX299475 1564 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 3 from Patent EP1154019.
ACCESSION AX299475
VERSION AX299475.1 GI:17129231
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bergsma,D.J. and Ellis,C.E.
TITLE G-protein coupled receptor (hfgan72x)
JOURNAL Patent: EP 1154019-A 3 14-NOV-2001;
SmithKline Beecham Corporation (US)
FEATURES Location/Qualifiers

source 1. .1564
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
Best Local Similarity 99.9%; Pred. No. 2.6e-209;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGAATTATCTG 120
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGAATTATCTG 273

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db 334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 393

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 300
Db 394 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 453

Qy 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCATGCCCTTGCAAG 360
Db 454 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCATGCCCTTGCAAG 513

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 633

Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 540
Db 634 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 693

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 753

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCAAGCTTCTCA 660
Db 754 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCAAGCTTCTCA 813

Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Db 814 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC 780
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 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC 933
 |||||||
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCAGCCCCGGGC 840
 |||||||
 Db 934 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCAGCCCCGGGC 993
 |||||||
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
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 Qy 901 ATGGTGGTGTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
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 Db 1054 ATGGTGGTGTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 1113
 |||||||
 Qy 961 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
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 Db 1114 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1173
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 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
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 Db 1174 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1233
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 Qy 1081 CTCAGTGG 1088
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 Db 1234 CTCAGTGG 1241

RESULT 13

AX549082

LOCUS AX549082 1564 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 367 from Patent WO02061087.
 ACCESSION AX549082
 VERSION AX549082.1 GI:25813851
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
 TITLE Antigenic peptides, such as for G protein-coupled receptors
 (GPCRs), antibodies thereto, and systems for identifying such
 antigenic peptides
 JOURNAL Patent: WO 02061087-A 367 08-AUG-2002;
 Lifespan Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. .1564
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 95.98; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.98; Pred. No. 2.6e-209;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	214	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	513
Qy	361	GTCATCCCTATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCTATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481	GCCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	540
Db	634	GCCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAGCGC	780
Db	874	AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993

Qy	841	CGCGCCTTCCGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCCTGGCTTCCGCCTCTGCTACCTGCCATCAGCGCCTCAATGCTT	960
Db	1054	ATGGTGGTGCCTGGCTTCCGCCTCTGCTACCTGCCATCAGCGCCTCAATGCTT	1113
Qy	961	AAGAGGGTGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTC	1020
Db	1114	AAGAGGGTGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTC	1173
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAAC	1080
Db	1174	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAAC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 14

AX746121

LOCUS	AX746121	1564 bp	DNA	linear	PAT 12-JUN-2003
DEFINITION	Sequence 4 from Patent EP1156110.				
ACCESSION	AX746121				
VERSION	AX746121.1	GI:31744927			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Bergsma, D.J. and Ellis, C.E.				
TITLE	G-protein coupled receptor (HFGAN72Y)				
JOURNAL	Patent: EP 1156110-A 4 21-NOV-2001; SMITHKLINE BEECHAM CORPORATION (US)				
FEATURES	Location/Qualifiers				
source	1. .1564 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /note="HGS EST 554692"				

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG	273

Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTC	393
Qy	241	ACCAAAC TACTT CATT GT CAAC CT GT CC CT GG CT GA CG TT CT GG T G ACT G CT AT CT GC CT G	300
Db	394	ACCAAAC TACTT CATT GT CAAC CT GT CC CT GG CT GA CG TT CT GG T G ACT G CT AT CT GC CT G	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481	GCCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGCTT	960
Db	1054	ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGCTT	1113

Qy 961 AAGAGGGTGGTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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 Db 1114 AAGAGGGTGGTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
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 Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
 |||||||
 Db 1174 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233
 |||||||
 Qy 1081 CTCAGTGG 1088
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 Db 1234 CTCAGTGG 1241

RESULT 15

AX840912

LOCUS AX840912 1564 bp DNA linear PAT 16-DEC-2003
 DEFINITION Sequence 8 from Patent WO03075945.
 ACCESSION AX840912
 VERSION AX840912.1 GI:39979051
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Eulenberg,K., Steuernagel,A., Haeder,T. and Broenner,G.
 TITLE Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750
 homologous proteins involved in the regulation of energy
 homeostasis
 JOURNAL Patent: WO 03075945-A 8 18-SEP-2003;
 DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;
 Forschung (DE)
 FEATURES Location/Qualifiers
 source 1. .1564
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
 |||||||
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
 |||||||
 Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 273
 |||||||
 Qy 121 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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 Db 274 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
 |||||||
 Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
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Db 334 CTGGTGGCAACACGCTGGCTGCCTGGCGTGCGGAACCACCATGAGGACAGTC 393
Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 394 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453
Qy 301 CGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTTCCGGCATGCCCTCTGCAAG 360
Db 454 CGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTTCCGGCATGCCCTCTGCAAG 513
Qy 361 GTCATCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 633
Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 540
Db 634 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 693
Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 753
Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db 754 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 813
Qy 661 ATTGTCACCTACCTGCCCACTGGCCTCATGGCATGGCTATTCAGATATTCCGC 720
Db 814 ATTGTCACCTACCTGCCCACTGGCCTCATGGCATGGCTATTCAGATATTCCGC 873
Qy 721 AAGCTCTGGGCCAGATCCCCGGCACCCACTCAGCACTGGTGCAGGAACGGC 780
Db 874 AAGCTCTGGGCCAGATCCCCGGCACCCACTCAGCACTGGTGCAGGAACGGC 933
Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGG 840
Db 934 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGG 993
Qy 841 CGCGCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 994 CGCGCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy 901 ATGGTGGTGTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGCTT 960
Db 1054 ATGGTGGTGTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGCTT 1113
Qy 961 AAGAGGGTGGATGTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Db 1114 AAGAGGGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1173
Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC 1080
Db 1174 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGG 1088
| | | | |
Db 1234 CTCAGTGG 1241

Search completed: October 15, 2004, 19:59:40
Job time : 4593.56 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:52:46 ; Search time 483.963 Seconds
(without alignments)
9945.416 Million cell updates/sec

Title: US-10-070-532-5

Perfect score: 1133

Sequence: 1 atggagccctcagccacccc.....tcctgaccatcggtccccgg 1133

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	1133	100.0	1133	4	AAS00493			Aas00493 Human neu
2	1131.4	99.9	1133	2	AAT42828			Aat42828 Neuropept
3	1131.4	99.9	1133	2	AAV68512			Aav68512 Nucleotid
4	1131.4	99.9	1133	6	ABA96020			Aba96020 HGS EST 5
5	1128.2	99.6	1170	2	AAV68511			Aav68511 Nucleotid
6	1128.2	99.6	1170	6	ABA96019			Aba96019 G-protein
7	1086.4	95.9	1564	2	AAV63468			Aav63468 cDNA enco

8	1086.4	95.9	1564	2	AAV68514	Aav68514 Nucleotid
9	1086.4	95.9	1564	4	AAF32103	Aaf32103 Human HFG
10	1086.4	95.9	1564	6	ABA96021	Aba96021 HGS EST 5
11	1086.4	95.9	1564	6	AAI64173	Aai64173 HFGAN72X
12	1086.4	95.9	1564	6	AAI64172	Aai64172 Human HFG
13	1086.4	95.9	1564	7	ABZ42789	Abz42789 Human ore
14	1084.8	95.7	1110	2	AAT42827	Aat42827 Neuropept
15	1084.8	95.7	1278	4	AAS00491	Aas00491 Human neu
16	1084.8	95.7	1564	4	AAS17464	Aas17464 Human G p
17	1083.2	95.6	1209	2	AAT42826	Aat42826 Neuropept
18	1081.6	95.5	1278	5	ABI98014	Abi98014 Non-endog
19	1076.8	95.0	1110	4	AAS00492	Aas00492 Human neu
20	1040	91.8	1278	4	AAD09335	Aad09335 Cynomolgo
21	912	80.5	1281	5	AAC85974	Aac85974 Dog orexi
22	670.6	59.2	789	2	AAT13909	Aat13909 Rabbit G-
23	670.6	59.2	789	2	AAT51065	Aat51065 G-protein
24	520.8	46.0	1633	2	AAX29700	Aax29700 Human 7-t
25	520.8	46.0	1843	7	ABZ42790	Abz42790 Human ore
26	516.2	45.6	1335	4	AAF90300	Aaf90300 Nucleotid
27	516	45.5	1335	5	ABI98015	Abi98015 Non-endog
28	249.2	22.0	344	5	AAF56748	Aaf56748 Human HCR
29	249.2	22.0	9785	5	AAF55159	Aaf55159 Nucleotid
30	249.2	22.0	10453	4	AAS17462	Aas17462 Human G p
31	244	21.5	244	4	AAS17449	Aas17449 Human G p
32	230	20.3	331	5	AAF56750	Aaf56750 Human HCR
33	225.4	19.9	227	4	AAS17453	Aas17453 Human G p
34	197.4	17.4	356	4	AAS17445	Aas17445 Human G p
35	197	17.4	452	5	AAF56746	Aaf56746 Human HCR
36	181	16.0	263	5	AAF56747	Aaf56747 Human HCR
37	179	15.8	179	4	AAS17447	Aas17447 Human G p
38	163.2	14.4	1290	3	AAA70507	Aaa70507 Novel hum
39	163.2	14.4	1290	3	AAA70508	Aaa70508 Novel hum
40	163.2	14.4	1290	4	AAH78518	Aah78518 Nucleotid
41	163.2	14.4	1290	4	AAH78519	Aah78519 Nucleotid
42	163.2	14.4	1290	7	ACC49315	Acc49315 Human RFR
43	163.2	14.4	1290	7	ACC49316	Acc49316 Human RFR
44	163.2	14.4	1290	9	ADB76179	Adb76179 Altenativ
45	163.2	14.4	1290	9	ADB76178	Adb76178 Human OT7

ALIGNMENTS

RESULT 1
 AAS00493
 ID AAS00493 standard; cDNA; 1133 BP.
 XX
 AC AAS00493;
 XX
 DT 17-MAY-2001 (first entry)
 XX
 DE Human neuropeptide receptor splice variant 2 cDNA.
 XX
 KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
 KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
 KW cardiovascular disorder; autoimmune disorder; infectious disorder;
 KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW protein co-ordinate data; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1119
FT /*tag= a
FT /product= "neuropeptide receptor splice variant 2"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR P-PSDB; AAU00440.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 4; Fig 3; 385pp; English.
XX
CC The present sequence encodes for human neuropeptide receptor splice
CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
CC described. The neuropeptide receptor shows sequence homology to the
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
CC neuropeptide receptor are useful for diagnosing, preventing, or treating
CC a pathological condition in a subject related to the central nervous and
CC peripheral nervous systems (CNS and PNS). The polypeptides and
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart
CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
CC diabetes mellitus. In particular they are useful for preventing, treating
CC or ameliorating a medical condition in a mammal such as obesity/eating
CC behaviour disorders, narcolepsy, neurological disease, addiction to
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
CC headaches and anxiety disorders. The polynucleotides encoding the
CC neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases
XX
SQ Sequence 1133 BP; 202 A; 367 C; 313 G; 251 T; 0 U; 0 Other;

Query Match 100.0%; Score 1133; DB 4; Length 1133;
Best Local Similarity 100.0%; Pred. No. 1.8e-263;
Matches 1133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGGCC 60

Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Qy	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Qy	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Db	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Qy	361 GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361 GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Qy	661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Qy	721 AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	780
Db	721 AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	780
Qy	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841 CGCGCTTCTGGCTGAAGTGAAGCAGATGGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTT 960
Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 2

AAT42828

ID AAT42828 standard; cDNA; 1133 BP.

XX

AC AAT42828;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-2 gene.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT misc_feature 1117. .1119

FT /*tag= a

FT /note= "In-frame stop codon"

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR P-PSDB; AAW06126.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify

PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.

XX

PS Disclosure; Page 52; 77pp; English.

xx

CC The sequence encodes human neuropeptide receptor splice variant-2, which
CC retains activity corresponding to the mature receptor (encoded by
CC AAT42826). The receptor gene has been isolated from a human adult
CC hypothalamus cDNA library, and is structurally related to the G-protein-
CC coupled receptor family. The receptor may be used in a drug screening
CC assay for isolation of receptor-agonists and -antagonists, which may be
CC used as anorectic, antitumour, anticholesterolemic, neuroprotective,
CC anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be
CC used in genetic disease diagnosis or gene therapy. The receptor and its
CC corresponding antibody may also be used in therapy and diagnosis

xx

SQ Sequence 1133 BP; 202 A; 368 C; 312 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 2; Length 1133;
 Best Local Similarity 99.9%; Pred. No. 4.5e-263;
 Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

QY 181 CTGGTGGCAACACGCTGGCTGCCTGGCCGTGGCGGAACCACCATGAGGACAGTC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Ph 181 CTGGTGGCAACACGCTGGCTGCCTGGCCGTGGCGGAACCACCATGAGGACAGTC 240

QY 241 ACCAACTACTTCATTGTCAACCTGTCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Pb 241 ACCAACTACTTCATTGTCAACCTGTCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

QY 301 CCGGCCAGCCTGCTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTCTGCAAG 360
|||
Pb 301 CCGCCGGAGCCTGCTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Eh 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGACTGGAAGCGC	780
Db	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	901	ATGGTGGTGGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC	1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCCTGACCATCGTGCCCCGG	1133
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCCTGACCATCGTGCCCCGG	1133

RESULT 3

AAV68512

ID AAV68512 standard; cDNA; 1133 BP.

XX

AC AAV68512;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HGS EST 557082.

XX

KW HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;
 KW probe; agonist; antagonist; activation; inhibition; gene therapy;
 KW antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;
 KW bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;
 KW hypertension; urinary retention; osteoporosis; angina pectoris;

KW myocardial infarction; ulcer; allergies; psychotic disorder;
KW neurological disorder; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN EP875565-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308554.
XX
PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Example 1; Page 18-19; 22pp; English.
XX
CC This is the nucleotide sequence of the HGS EST 557082 used in the method
CC of the invention involving the G-protein coupled receptor, HFGAN72Y. Its
CC polypeptides and polynucleotides are useful for diagnosing susceptibility
CC to diseases by detecting mutations in the HFGAN72Y gene using probes
CC containing the HFGAN72Y nucleotide sequence, and can diagnose diseases
CC associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or
CC mRNA expression levels. Agonists/antagonists can be used in treatment to
CC activate/inhibit HFGAN72Y activity, in addition to direct administration
CC of antisense sequences to prevent expression, or HFGAN72Y polypeptides to
CC treat conditions associated with a lack HFGAN72Y protein. Gene therapy
CC may also be used to affect endogenous HFGAN72Y polypeptide production.
CC HFGAN72Y antibodies are useful for inducing an immune response to
CC immunise and prevent diseases, and for isolating HFGAN72Y clones or
CC purifying the polypeptides by affinity chromatography. HFGAN72Y
CC polypeptides can be administered directly or as a vaccine to inoculate
CC against diseases. Diseases diagnosed, prevented or treated include HIV-1
CC or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC ulcers; allergies, benign prostatic hypertrophy, and psychotic and
CC neurological disorders. The HFGAN72Y polypeptide is also useful for
CC mapping the gene to a chromosome, allowing gene inheritance to be studied
CC through linkage analysis.
XX
SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 2; Length 1133;
 Best Local Similarity 99.9%; Pred. No. 4.5e-263;
 Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
|||||

Db 1 ATGGAGCCCTCAGCCACCCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTTCGTCGTGCC 180
Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTTCGTCGTGCC 180
Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Db 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
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Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
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Qy 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGGAACTGGAAGCGC 780
Db 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGGAACTGGAAGCGC 780
Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Qy 841 CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 841 CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
|||
Db 901 ATGGTGGTGCCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
|||
Db 961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
|||
Db 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080

Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
|||
Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 4

ABA96020

ID ABA96020 standard; cDNA; 1133 BP.

XX

AC ABA96020;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 557082.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW schizophrenia; manic depression; dementia; mental retardation; EST;
KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW HGS EST 557082; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

XX

PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological

PT disorders.

XX

PS Example 1; Page 18-19; 22pp; English.

XX

CC The sequence represents HGS EST 557082. The invention relates to a novel
CC isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of
CC the invention has cytostatic, cardiant, analgesic, tranquillising,
CC nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has
CC a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y
CC polypeptide agonist are used to treat a subject in need of enhanced
CC HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or
CC nucleic acid which inhibits HFGAN72Y expression is used to treat a
CC subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-
CC associated diseases include infections, particularly by HIV-1 or HIV-2,
CC pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,
CC ulcers, urinary retention, asthma, allergies, benign prostatic
CC hypertrophy, and psychotic and neurological disorders including anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation and dyskinesias such as Huntington's disease and Tourette's
CC syndrome

XX

SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;
Best Local Similarity 99.9%; Pred. No. 4.5e-263;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db |||||||

Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Db |||||||

Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db |||||||

Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGCGGAACCACACATGAGGACAGTC 240
Db |||||||

Db 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGCGGAACCACACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db |||||||

Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CGGGCCAGCCTGCTGGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
Db |||||||

Db 301 CGGGCCAGCCTGCTGGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db |||||||

Db 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGGG 480
Db |||||||

Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 480
Qy	481	GCCC GTGG CTCC AT CCTGGGCATCTGGGCTGTGCGCTGCCATCATGGT GCCCCAGGCT 540
Db	481	GCCC GTGG CTCC AT CCTGGGCATCTGGGCTGTGCGCTGCCATCATGGT GCCCCAGGCT 540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC 720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC 720
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCA CCTCAGCACTGGT GCGGA ACTGGAAGCGC 780
Db	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCA CCTCAGCACTGGT GCGGA ACTGGAAGCGC 780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900
Qy	901	ATGGTGGT GCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
Db	901	ATGGTGGT GCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
Qy	961	AAGAGGGT GTT CGGGAT GTT CCGCC AAGCCAGTGACCGCGAAGCTGTCTACGCC TGCTC 1020
Db	961	AAGAGGGT GTT CGGGAT GTT CCGCC AAGCCAGTGACCGCGAAGCTGTCTACGCC TGCTC 1020
Qy	1021	ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
Db	1021	ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGCTGACCATCGT GCCCCGG 1133
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGCTGACCATCGT GCCCCGG 1133

RESULT 5

AAV68511

ID AAV68511 standard; cDNA; 1170 BP.

XX

AC AAV68511;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HFGAN72Y: a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;
KW antagonist; activation; inhibition; gene therapy; antibody;
KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;
KW asthma; Parkinson's disease; acute heart failure; hypotension;
KW hypertension; urinary retention; osteoporosis; angina pectoris;
KW myocardial infarction; ulcer; allergies; psychotic disorder;
KW neurological disorder; gene mapping; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1170
FT /*tag= a
FT /product= "HFGAN72Y protein"
XX
PN EP875565-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308554.
XX
PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
DR P-PSDB; AAW80805.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Claim 3; Page 7; 22pp; English.
XX
CC This is the nucleotide sequence of the G-protein coupled receptor,
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases by
CC detecting mutations in the HFGAN72Y gene using probes containing the
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC HFGAN72Y activity, in addition to direct administration of antisense
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC administered directly or as a vaccine to inoculate against diseases.
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene

CC to a chromosome, allowing gene inheritance to be studied through linkage
CC analysis

XX

SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 99.6%; Score 1128.2; DB 2; Length 1170;
Best Local Similarity 99.7%; Pred. No. 2.7e-262;
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db |||||||
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Db |||||||
Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db |||||||
Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db |||||||
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db |||||||
Qy 301 CGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG 360
Db |||||||
Qy 361 GTCATCCCCTATCTACAGGCTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db |||||||
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGG 480
Db |||||||
Qy 481 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db |||||||
Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTTCTCA 600
Db |||||||
Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCAACAGTTGCTTCTT 660
Db |||||||
Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Db |||||||

Qy	721 AAGCTCTGGGGCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGC GG GA CT GGAAGCGC 780
Db	721 AAGCTCTGGGGCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGC GG GA CT GGAAGCGC 780
Qy	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCAGCCCCGGGC 840
Db	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCAGCCCCGGGC 840
Qy	841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db	841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy	901 ATGGTGGTGC T GTGGTCTTCGCC T CTGCTAC T GCCATCAGCGC T C T CAATGTC C TT 960
Db	901 ATGGTGGTGC T GTGGTCTTCGCC T CTGCTAC T GCCATCAGCGC T C T CAATGTC C TT 960
Qy	961 AAGAGGGTGGT C GGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGT T ACGCC T GCTTC 1020
Db	961 AAGAGGGTGGT C GGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGT T ACGCC T GCTTC 1020
Qy	1021 ACCTTCTCCC A CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAAC T TC 1080
Db	1021 ACCTTCTCCC A CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAAC T TC 1080
Qy	1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGCT C TGACC A CGT T GCC C GG 1133
Db	1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGCTGCC A CGT T GCC C GG 1133

RESULT 6

ABA96019

ID ABA96019 standard; cDNA; 1170 BP.

XX

AC ABA96019;

XX

DT 12-MAR-2002 (first entry)

XX

DE G-protein coupled receptor (HFGAN72Y) cDNA.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer; KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy; KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer; KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder; KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium; KW schizophrenia; manic depression; dementia; mental retardation; KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1170

FT /*tag= a

FT /product= "HGFAN72Y"

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX
PF 27-OCT-1997; 2001EP-00203010.
XX
PR 30-APR-1997; 97US-00846705.
PR 27-OCT-1997; 97EP-00308554.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-084320/12.
DR P-PSDB; ABB08208.
XX
PT New polynucleotide encoding a G-protein coupled receptor designated HFGAN72Y is useful to diagnose and treat associated diseases including cancer, infection, cardiac disease and psychotic and neurological disorders.
XX
PS Claim 3; Page 7; 22pp; English.
XX
CC The sequence encodes G-protein coupled receptor HFGAN72Y. The invention relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic, cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or nucleic acid which inhibits HFGAN72Y expression is used to treat a subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-associated diseases include infections, particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers, ulcers, urinary retention, asthma, allergies, benign prostatic hypertrophy, and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease and Tourette's syndrome
XX
SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 99.6%; Score 1128.2; DB 6; Length 1170;
Best Local Similarity 99.7%; Pred. No. 2.7e-262;
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db |||||||
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
Qy 121 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Db 121 TACCCAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db |||||||

Db	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Db	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTTCTGGCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTTCTGGCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	601	GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Qy	661	ATTGTCACCTACCTGCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCAGATCCCCGGCACCCACTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Db	721	AAGCTCTGGGCCAGATCCCCGGCACCCACTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841	CGCGCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGCTTT	960
Db	901	ATGGTGGTGTGCTGGCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGCTTT	960
Qy	961	AAGAGGGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080

Qy 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG 1133

RESULT 7

AAV63468

ID AAV63468 standard; cDNA; 1564 BP.

XX

AC AAV63468;

XX

DT 26-JAN-1999 (first entry)

XX

DE cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154. .1431

FT /*tag= a

FT /product= "HFGAN72X"

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 1998-559432/48.

DR P-PSDB; AAW80456.

XX

PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.

XX

PS Claim 3; Page 7; 24pp; English.

XX

CC The present sequence encodes a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,

CC asthma, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
 CC and psychotic and neurological disorders
 XX
 SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

 Query Match 95.9%; Score 1086.4; DB 2; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 3.6e-252;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
 |||||||
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

 Qy 61 TCCCCGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
 |||||||
 Db 214 TCCCCGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 273

 Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
 |||||||
 Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

 Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
 |||||||
 Db 334 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 393

 Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
 |||||||
 Db 394 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453

 Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCATGCCCTTGCAAG 360
 |||||||
 Db 454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCATGCCCTTGCAAG 513

 Qy 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
 |||||||
 Db 514 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480
 |||||||
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 633

 Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGTGGCATCATGGTCCCCAGGCT 540
 |||||||
 Db 634 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGTGGCATCATGGTCCCCAGGCT 693

 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTTCTCA 600
 |||||||
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTTCTCA 753

 Qy 601 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCAAGCTTCTCA 660
 |||||||
 Db 754 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCAAGCTTCTCA 813

 Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCAGATGGCTATTCCAGATATTCCGC 720
 |||||||

Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 873
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCGC 780
 |||||
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCGC 933
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||
 Db 934 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 993
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 |||||
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
 Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCTT 960
 |||||
 Db 1054 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCTT 1113
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
 |||||
 Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1173
 Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
 |||||
 Db 1174 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1233
 Qy 1081 CTCAGTGG 1088
 |||||
 Db 1234 CTCAGTGG 1241

RESULT 8

AAV68514

ID AAV68514 standard; cDNA; 1564 BP.

XX

AC AAV68514;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of a probe HGS EST 554692.

XX

KW Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;
 KW mutation; probe; agonist; antagonist; activation; inhibition;
 KW gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; ulcer; allergies;
 KW psychotic disorder; neurological disorder; gene mapping; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX
PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC This is the nucleotide sequence of the probe HGS EST 554692 used in the
CC method of the invention involving the G-protein coupled receptor,
CC HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing
CC susceptibility to diseases by detecting mutations in the HFGAN72Y gene
CC using probes containing the HFGAN72Y nucleotide sequence, and can
CC diagnose diseases associated with HFGAN72Y imbalance by determining
CC HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can
CC be used in treatment to activate/inhibit HFGAN72Y activity, in addition
CC to direct administration of antisense sequences to prevent expression, or
CC HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y
CC protein. Gene therapy may also be used to affect endogenous HFGAN72Y
CC polypeptide production. HFGAN72Y antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC HFGAN72Y clones or purifying the polypeptides by affinity chromatography.
CC HFGAN72Y polypeptides can be administered directly or as a vaccine to
CC inoculate against diseases. Diseases diagnosed, prevented or treated
CC include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders. The HFGAN72Y polypeptide is
CC also useful for mapping the gene to a chromosome, allowing gene
CC inheritance to be studied through linkage analysis
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 2; Length 1564;
Best Local Similarity 99.9%; Pred. No. 3.6e-252;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 213

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy 121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCGTGTTCGTCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCGTGTTCGTCGTGGCC 333

Qy	181	CTGGTGGGAAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334	CTGGTGGGAAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG	513
Qy	361	GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481	GCCC GTGGCTCCATCCTGGC ATCTGGGCTGTGTCGCTGGC ATCATGGT GCCCAGGCT	540
Db	634	GCCC GTGGCTCCATCCTGGC ATCTGGGCTGTGTCGCTGGC ATCATGGT GCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGT CACCTACCTGGCCCCACTGGCCTCATGGC ATGGC TATTCCAGA TATTCCGC	720
Db	814	ATTGT CACCTACCTGGCCCCACTGGCCTCATGGC ATGGC TATTCCAGA TATTCCGC	873
Qy	721	AAGCTCTGGGCCCGCAGATCCCCGGCACCCACTCAGCACTGGTGC GGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGCCCGCAGATCCCCGGCACCCACTCAGCACTGGTGC GGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGT GCTGGTCTGGCTTGCCTCTGCTACCTGCCATCAGCGT CCTCAATGTCCTT	960
Db	1054	ATGGTGGT GCTGGTCTGGCTTGCCTCTGCTACCTGCCATCAGCGT CCTCAATGTCCTT	1113
Qy	961	AAGAGGGT GTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	1114	AAGAGGGT GTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1173
Qy	1021	ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATACAACCTTC	1080

Db 1174 ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233
Qy 1081 CTCAGTGG 1088
| | | | |
Db 1234 CTCAGTGG 1241

RESULT 9

AAF32103

ID AAF32103 standard; cDNA; 1564 BP.

XX

AC AAF32103;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor coding sequence SEQ ID NO: 12.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;
KW truncation mutant; ligand; neurodegenerative disorder; pain;
KW eating disorder; behaviour disorder; mood disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;

XX

DR WPI; 2001-071483/08.

XX

PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.

XX

PS Disclosure; Fig 6; 101pp; English.

XX

CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions

XX

SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 4; Length 1564;
Best Local Similarity 99.9%; Pred. No. 3.6e-252;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	214	TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241	ACCAAACACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Db	394	ACCAAACACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	513
Qy	361	GTCATCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCATCATGGTCCCCAGGCT	540
Db	634	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993

Qy	841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG .900
Db	994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy	901 ATGGTGGTGCTGCTGGTCTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT 960
Db	1054 ATGGTGGTGCTGCTGGTCTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT 1113
Qy	961 AAGAGGGTGGTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Db	1114 AAGAGGGTGGTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1173
Qy	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
Db	1174 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1233
Qy	1081 CTCAGTGG 1088
Db	1234 CTCAGTGG 1241

RESULT 10

ABA96021

ID ABA96021 standard; cDNA; 1564 BP.

XX

AC ABA96021;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 554692.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer; nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy; infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer; cardiac disease; urinary retention; asthma; allergy; psychotic disorder; benign prostatic hypertrophy; neurological disorder; anxiety; delirium; schizophrenia; manic depression; dementia; mental retardation; EST; dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; HGS EST 554692; expressed sequence tag; probe; ss.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

XX
PT New polynucleotide encoding a G-protein coupled receptor designated HFGAN72Y is useful to diagnose and treat associated diseases including cancer, infection, cardiac disease and psychotic and neurological disorders.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC The sequence represents HGS EST 554692. The sequence was used in the invention as a probe to screen a human genomic placenta phage library. CC The invention relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic, CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y CC expression is used to treat a subject in need of decreased HFGAN72Y CC activity or expression. HFGAN72Y-associated diseases include infections, CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma, CC allergies, benign prostatic hypertrophy, and psychotic and neurological CC disorders including anxiety, schizophrenia, manic depression, delirium, CC dementia, severe mental retardation and dyskinesias such as Huntington's CC disease and Tourette's syndrome
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
Best Local Similarity 99.9%; Pred. No. 3.6e-252;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
Db 214 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 273

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCGTGTGGCGTGGCC 333

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db 334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 393

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360
Db 454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 513

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGTTCATC 420

Db	514	 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	480
Db	574	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	633
Qy	481	 GCCCGTGGCTCCATCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	634	 GCCCGTGGCTCCATCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	693
Qy	541	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Db	814	 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	873
Qy	721	 AAGCTCTGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCAGAACGGCAGCGC	780
Db	874	 AAGCTCTGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCAGAACGGCAGCGC	933
Qy	781	 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGG	840
Db	934	 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGG	993
Qy	841	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	 ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	1054	 ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	1113
Qy	961	 AAGAGGGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	1114	 AAGAGGGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1173
Qy	1021	 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC	1080
Db	1174	 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC	1233
Qy	1081	 CTCAGTGG 1088	
Db	1234	 CTCAGTGG 1241	

RESULT 11

AAI64173

ID AAI64173 standard; cDNA; 1564 BP.

XX

AC AAI64173;

XX
DT 22-JAN-2002 (first entry)
XX
DE HFGAN72X G coupled receptor polypeptide partial sequence.
XX
KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; probe;
KW myocardial infarction; ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154. .1362
FT /*tag= a
FT /partial
FT /product= "HFGAN72X protein"
FT /note= "The specification states that this is a partial
FT sequence even though it contains start and stop codons;
FT HFGAN72X is a G coupled receptor polypeptide"
FT /transl_except= (pos:991. .993, aa:Ala)
XX
PN EP1154019-A2.
XX
PD 14-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203008.
XX
PR 30-APR-1997; 97US-00846704.
PR 27-OCT-1997; 97EP-00308563.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-012659/02.
DR P-PSDB; AAG78346.
XX
PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.
XX
PS Example 3; Page 9; 24pp; English.
XX
CC The present sequence is that of a known partial nucleotide sequence
CC encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify
CC the HFGAN72X gene (AAI64173). The specification describes a newly
CC isolated polynucleotide encoding a human HFGAN72X G coupled receptor
CC polypeptide. The protein of the invention has antibacterial, fungicide,
CC virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,
CC nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,
CC neuroleptic, antidepressant, anticonvulsant and osteopathic activities.

CC HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to
CC treat diseases requiring increased activity or expression of HFGAN72X;
CC for recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and
CC dyskinesias

XX

SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
Best Local Similarity 99.9%; Pred. No. 3.6e-252;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 154 ATGGAGCCCTCAGCCACCCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 273

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 333

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db 334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 393

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 300
Db 394 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 453

Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGACTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360
Db 454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 513

Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 633

Qy	481	GCCC GTGG CTCC ATCT GGGC ATCT GGGCT GTGTC GCTGG CCACTATGGT GCCCC AGGCT	540
Db	634	GCCC GTGG CTCC ATCT GGGC ATCT GGGCT GTGTC GCTGG CCACTATGGT GCCCC AGGCT	693
Qy	541	GCAGT CATGGA ATGC AGCAGT GTGCT GCCTGAGCTAGCCA ACCGCACACGGCTTTCTCA	600
Db	694	GCAGT CATGGA ATGC AGCAGT GTGCT GCCTGAGCTAGCCA ACCGCACACGGCTTTCTCA	753
Qy	601	GTCT GTGATG AACGCT GGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCT GTGATG AACGCT GGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGT CACCTACCTGGCCCCACTGGCCTCATGCCATGGCTATTCCAGATATTCCGC	720
Db	814	ATTGT CACCTACCTGGCCCCACTGGCCTCATGCCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCCGCAGATCCCCGGCACCACCTCAGCACTGGT GCGGA CTGGAAGCGC	780
Db	874	AAGCTCTGGGCCCGCAGATCCCCGGCACCACCTCAGCACTGGT GCGGA CTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTT CCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTT CCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGT GCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGT CCTCAATGTCCTT	960
Db	1054	ATGGTGGT GCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGT CCTCAATGTCCTT	1113
Qy	961	AAGAGGGT GTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	1114	AAGAGGGT GTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1173
Qy	1021	ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 12

AAI64172

ID AAI64172 standard; cDNA; 1564 BP.

XX

AC AAI64172;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide cDNA.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;

KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;

KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154..1431
FT /*tag= a
FT /product= "HFGAN72X protein"
FT /note= "G coupled receptor polypeptide"
XX
PN EP1154019-A2.
XX
PD 14-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203008.
XX
PR 30-APR-1997; 97US-00846704.
PR 27-OCT-1997; 97EP-00308563.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-012659/02.
DR P-PSDB; AAG78345.
XX
PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.
XX
PS Claim 3; Page 7; 24pp; English.
XX
CC The present sequence is that of a cDNA encoding a HFGAN72X polypeptide
CC (AAG78345). The specification describes a newly isolated polynucleotide
CC encoding a HFGAN72X G coupled receptor polypeptide. The protein of the
CC invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,
CC cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,
CC antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant
CC and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to
CC express HFGAN72X in vivo, to treat diseases requiring increased activity
CC or expression of HFGAN72X; for recombinant production of HFGAN72X;
CC diagnose diseases (or susceptibility to them) by detecting mutations in
CC genomic sequences and in chromosome identification and mapping. HFGAN72X
CC polypeptides are used to raise specific antibodies; as therapeutic agents
CC ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X
CC proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to
CC identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids
CC that inhibit expression of HFGAN72X and polypeptides that compete with
CC ligands for binding to HFGAN72X proteins are also useful therapeutically
CC and diagnostically. HFGAN72X-related diseases include infections
CC (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;

CC cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;
 CC hypotension; hypertension; urinary retention; osteoporosis; angina
 CC pectoris; myocardial infarction; ulcers; asthma; allergy; benign
 CC prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium
 CC ; dementia; severe mental retardation and dyskinesias
 XX
 SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;
 Query Match 95.9%; Score 1086.4; DB 6; Length 1564;
 Best Local Similarity 99.9%; Pred. No. 3.6e-252;
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
 |||||||
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
 |||||||
 Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
 |||||||
 Db 214 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 273
 |||||||
 Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
 |||||||
 Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 333
 |||||||
 Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACATGAGGACAGTC 240
 |||||||
 Db 334 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACATGAGGACAGTC 393
 |||||||
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
 |||||||
 Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453
 |||||||
 Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360
 |||||||
 Db 454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 513
 |||||||
 Qy 361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 420
 |||||||
 Db 514 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 573
 |||||||
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
 |||||||
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 633
 |||||||
 Qy 481 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCATCTGGTCCCCAGGCT 540
 |||||||
 Db 634 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCATCTGGTCCCCAGGCT 693
 |||||||
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTCTCA 600
 |||||||
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTCTCA 753
 |||||||
 Qy 601 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
 |||||||
 Db 754 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 813
 |||||||
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC	780
Db	874	AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1173
Qy	1021	ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 13

ABZ42789

ID ABZ42789 standard; DNA; 1564 BP.

XX

AC ABZ42789;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 nucleotide SEQ ID NO:367.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR P-PSDB; ABP81941.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
CJ
XX
SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 7; Length 1564;
Best Local Similarity 99.9%; Pred. No. 3.6e-252;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGGCGTATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGGCGTATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	333
Qy	181	CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	334	CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	393
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGCCATGCCCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGCCATGCCCTGCAAG	513
Qy	361	GTCATCCCCATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCATCTACAGGCTGTGTCGTGAGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG	633
Qy	481	GCCCCTGGCTCCATCCTGGCATCTGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	540
Db	634	GCCCCTGGCTCCATCCTGGCATCTGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	814	ATTGTACCTACCTGGCCCCACTGGGCTCATGGCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGCGC	780
Db	874	AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960

Db 1054 ATGGTGGTGCCTGCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCCT 1113
Qy 961 AAGAGGGTGGTGCCTGCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCCT 1020
Db 1114 AAGAGGGTGGTGCCTGCTGGCTTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCCT 1173
Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
Db 1174 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233
Qy 1081 CTCAGTGG 1088
Db 1234 CTCAGTGG 1241

RESULT 14

AAT42827

ID AAT42827 standard; cDNA; 1110 BP.

XX

AC AAT42827;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1 gene.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;
KW receptor-agonist; receptor-antagonist; anorectic; antitumour;
KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
KW sedative; diagnostic; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR P-PSDB; AAW06125.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.

XX

PS Disclosure; Page 50-51; 77pp; English.

XX

CC The sequence encodes human neuropeptide receptor splice variant-1, which
CC retains activity corresponding to the mature receptor (encoded by
CC AAT42826). The receptor gene has been isolated from a human adult

CC hypothalamus cDNA library, and is structurally related to the G-protein-coupled receptor family. The receptor may be used in a drug screening assay for isolation of receptor-agonists and -antagonists, which may be used as anorectic, antitumour, anticholesterolemic, neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be used in genetic disease diagnosis or gene therapy. The receptor and its corresponding antibody may also be used in therapy and diagnosis

XX

SQ Sequence 1110 BP; 194 A; 364 C; 305 G; 247 T; 0 U; 0 Other;

Query Match 95.7%; Score 1084.8; DB 2; Length 1110;
Best Local Similarity 99.8%; Pred. No. 7.9e-252;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Qy	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGGCTGGCCATGCCCTCTGCAAG 360
Db	301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGGCTGGCCATGCCCTCTGCAAG 360
Qy	361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db	361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTGCCAGGCT 540
Db	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTGCCAGGCT 540
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTTCTCA 600
Db	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACAGGCTTTCTCA 600
Qy	601 GTCTGTGATGAAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db	601 GTCTGTGATGAAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy	661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Db	661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Qy	721 AAGCTCTGGGGCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Db	721 AAGCTCTGGGGCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Qy	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGGTCTCAATGCTTT	960
Db	901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTCCCCATCAGGTCTCAATGCTTT	960
Qy	961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Qy	1081 CTCAGTGG 1088	
Db	1081 CTCAGTGG 1088	

RESULT 15

AAS00491

ID AAS00491 standard; cDNA; 1278 BP.

XX

AC AAS00491;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor cDNA.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
 KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
 KW cardiovascular disorder; autoimmune disorder; infectious disorder;
 KW eating behaviour disorder; narcolepsy; neurological disease;
 KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
 KW protein co-ordinate data; chromosome 1; ss.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT CDS 1. .1278

FT /*tag= a

FT /product= "neuropeptide receptor"

XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR P-PSDB; AAU00438.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 4; Fig 1; 385pp; English.
XX
CC The present sequence encodes for a novel human neuropeptide receptor
CC which shows sequence homology to the neuropeptide Y receptor. Two splice
CC variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
CC mutant (AAU00442) are also described. Polypeptides and polynucleotides of
CC the neuropeptide receptor are useful for diagnosing, preventing, or
CC treating a pathological condition in a subject related to the central
CC nervous and peripheral nervous systems (CNS and PNS). The polypeptides
CC and polynucleotides may be used to treat hyperproliferative,
CC cardiovascular, autoimmune, nervous system or infectious disorders e.g.
CC cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV
CC infection and diabetes mellitus. In particular they are useful for
CC preventing, treating or ameliorating a medical condition in a mammal such
CC as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC migraine headaches and anxiety disorders. The polynucleotides encoding
CC the neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases
XX
SQ Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

Query Match 95.7%; Score 1084.8; DB 4; Length 1278;
Best Local Similarity 99.8%; Pred. No. 8.2e-252;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
|||
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG 120
|||
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
|||
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241	ACCAAAC TACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241	ACCAAAC TACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
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Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG	480
Qy	481	GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTATCCAAAGATCTACCACAGTTGCTTCTT	660
Db	601	GTCTGTGATGAACGCTGGCAGATGACCTATCCAAAGATCTACCACAGTTGCTTCTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC 780	
Db	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC 780	
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGCTT	960
Db	901	ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGCTT	960
Qy	961	AAGAGGGTGGTGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGGTGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1020

Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
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Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy 1081 CTCAGTGG 1088
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Db 1081 CTCAGTGG 1088

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Job time : 485.963 secs

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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:25:17 ; Search time 88.8123 Seconds
(without alignments)
7079.645 Million cell updates/sec

Title: US-10-070-532-5

Perfect score: 1133

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1131.4	99.9	1133	2	US-08-846-705-3	Sequence 3, Appli
2	1131.4	99.9	1133	5	PCT-US95-05616-5	Sequence 5, Appli
3	1128.2	99.6	1170	2	US-08-846-705-1	Sequence 1, Appli
4	1114.4	98.4	1116	4	US-08-462-509B-5	Sequence 5, Appli
5	1086.4	95.9	1209	4	US-08-462-509B-1	Sequence 1, Appli
6	1086.4	95.9	1564	2	US-08-846-705-4	Sequence 4, Appli
7	1086.4	95.9	1564	3	US-08-846-704-1	Sequence 1, Appli
8	1086.4	95.9	1564	3	US-08-846-704-3	Sequence 3, Appli
9	1084.8	95.7	1110	4	US-08-462-509B-3	Sequence 3, Appli
10	1081.6	95.5	1209	5	PCT-US95-05616-1	Sequence 1, Appli

11	1076.8	95.0	1110	5	PCT-US95-05616-3	Sequence 3, Appli
12	697.6	61.6	843	3	US-08-513-974B-375	Sequence 375, App
13	670.6	59.2	789	3	US-08-513-974B-55	Sequence 55, Appl
14	670.6	59.2	789	4	US-09-461-436B-55	Sequence 55, Appl
15	520.8	46.0	1633	3	US-09-119-788-1	Sequence 1, Appli
16	249.2	22.0	9785	4	US-09-479-128-1	Sequence 1, Appli
17	163.2	14.4	1293	3	US-09-255-368-7	Sequence 7, Appli
18	156.2	13.8	1410	3	US-09-255-368-1	Sequence 1, Appli
19	128.4	11.3	168575	4	US-09-426-290-1	Sequence 1, Appli
20	119	10.5	1110	3	US-08-513-974B-31	Sequence 31, Appl
21	119	10.5	1110	3	US-08-776-971-26	Sequence 26, Appl
22	119	10.5	1110	4	US-09-461-436B-31	Sequence 31, Appl
23	119	10.5	1331	3	US-08-513-974B-322	Sequence 322, App
24	119	10.5	1331	3	US-08-776-971-103	Sequence 103, App
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26	108.8	9.6	669	3	US-08-776-971-99	Sequence 99, Appl
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28	108.8	9.6	1113	4	US-09-799-955-1	Sequence 1, Appli
29	103.2	9.1	1110	4	US-09-170-496D-25	Sequence 25, Appl
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31	103.2	9.1	1344	4	US-09-016-434-1295	Sequence 1295, Ap
32	103.2	9.1	1356	1	US-07-978-892A-4	Sequence 4, Appli
33	103.2	9.1	1535	4	US-09-016-434-1051	Sequence 1051, Ap
34	103.2	9.1	1969	1	US-07-937-609-28	Sequence 28, Appl
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36	100	8.8	2243	1	US-07-937-609-15	Sequence 15, Appl
37	100	8.8	2243	3	US-08-029-170-15	Sequence 15, Appl
38	98.4	8.7	1621	1	US-08-722-001-13	Sequence 13, Appl
39	98.4	8.7	1776	1	US-08-722-001-29	Sequence 29, Appl
40	98.4	8.7	2002	4	US-09-016-434-1172	Sequence 1172, Ap
41	98.4	8.7	2140	1	US-08-334-698-1	Sequence 1, Appli
42	98.4	8.7	2140	1	US-08-228-932-1	Sequence 1, Appli
43	98.4	8.7	2140	1	US-08-468-939-1	Sequence 1, Appli
44	98.4	8.7	2140	2	US-08-406-855A-1	Sequence 1, Appli
45	98.4	8.7	2140	2	US-08-722-190-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-846-705-3

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; Sequence 3, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: RATNER & PRESTIA
;     STREET: P.O. BOX 980
;     CITY: VALLEY FORGE
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;     COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-846-705-3

Query Match 99.9%; Score 1131.4; DB 2; Length 1133;
Best Local Similarity 99.9%; Pred. No. 9.6e-261;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Qy	361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420

Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGTAACCTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	480
Db	421	GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	480
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCCATGGCTATTCCAGATATTCCGC	720
Db	661	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCCATGGCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCAGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCAGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCTCAATGTCCTT	960
Db	901	ATGGTGGTGCCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCTCAATGTCCTT	960
Qy	961	AAGAGGGTGGATGTTCCGCCAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGGATGTTCCGCCAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGCTGACCATCGTCCCCGG	1133
Db	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGCTGACCATCGTCCCCGG	1133

RESULT 2

PCT-US95-05616-5

; Sequence 5, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-5

Query Match 99.9%; Score 1131.4; DB 5; Length 1133;
Best Local Similarity 99.9%; Pred. No. 9.6e-261;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
|||
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120
|||
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGCTCGTGGCC 180
|||
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGCTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
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Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
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Db	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
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Db	301	CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
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Db	421	GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG	480
Qy	481	GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCATCATGGTCCCCAGGGT	540
Db	481	GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCATCATGGTCCCCAGGGT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTA	600
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Qy	661	ATTGTACACTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	661	ATTGTACACTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCG	780
Db	721	AAGCTCTGGGCCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCG	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGCTTT	960
Db	901	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGCTTT	960
Qy	961	AAGAGGGTTCGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC	1020
Db	961	AAGAGGGTTCGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Qy	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGCTGACCATCGTCCCCGG	1133
Db	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGCTGACCATCGTCCCCGG	1133

RESULT 3
US-08-846-705-1
; Sequence 1, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-1

Query Match 99.6%; Score 1128.2; DB 2; Length 1170;
Best Local Similarity 99.7%; Pred. No. 5.6e-260;
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGATTATCTG 120

Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Qy	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Qy	481	GCCC GTGGCTCCATCTGGC ATCTGGGCTGTGTCGCTGGC CATCATGGT GCCCCAGGCT	540
Db	481	GCCC GTGGCTCCATCTGGC ATCTGGGCTGTGTCGCTGGC CATCATGGT GCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCTCATGGCCATGGCCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGCCAGATCCCCGGCACCA CCTCAGCACTGGTGC GGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGCCAGATCCCCGGCACCA CCTCAGCACTGGTGC GGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGTCTCGCCCTTGCTACCTGCCATCAGCGTCTCAATGTCCTT	960
Db	901	ATGGTGGTGTGCTGGTCTCGCCCTTGCTACCTGCCATCAGCGTCTCAATGTCCTT	960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGC~~GAAGCTGT~~TACGCCTGCTTC 1020
Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGC~~GAAGCTGT~~TACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCC~~ACTGGCTGGTGTACGCCAACAGCGCTGCCA~~ACCCCCATCATCTACAAC~~TT~~C 1080
Db 1021 ACCTTCTCCC~~ACTGGCTGGTGTACGCCAACAGCGCTGCCA~~ACCCCCATCATCTACAAC~~TT~~C 1080

Qy 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGT~~GCCCCGG~~ 1133
Db 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGT~~GCCCCGG~~ 1133

RESULT 4

US-08-462-509B-5

; Sequence 5, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 1..1116
US-08-462-509B-5

Db 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC 780
Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db 781 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 841 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCC 960
Db 901 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCC 960
Qy 961 AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Db 961 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 961 AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
Db 1021 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080
Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
Db 1081 ||||||| ||||||| ||||||| |||||||
Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116

RESULT 5

US-08-462-509B-1

; Sequence 1, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1209
US-08-462-509B-1

Query Match 95.9%; Score 1086.4; DB 4; Length 1209;
Best Local Similarity 99.9%; Pred. No. 5.2e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Qy	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG	360
Db	301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG	360
Qy	361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Qy	481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600

Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTCTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Qy	841	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCTCTCAATGTCCCT	960
Db	901	ATGGTGGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGCTCTCAATGTCCCT	960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGG 1088	
Db	1081	CTCAGTGG 1088	

RESULT 6

US-08-846-705-4

; Sequence 4, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; . APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER &

; STREET: P.O. BOX 98

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READA

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-846-705-4

Query Match 95.9%; Score 1086.4; DB 2; Length 1564;
Best Local Similarity 99.9%; Pred. No. 5.6e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61 TCCCCGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	214 TCCCCGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	273
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC	180
Db	274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC	333
Qy	181 CTGGTGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	334 CTGGTGGCAACACGCTGGTCTGCCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	393
Qy	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	454 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	513
Qy	361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420

Db	514	 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	 GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGG	480
Db	574	 GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGG	633
Qy	481	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	634	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	693
Qy	541	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGTTCTTT	660
Db	754	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGTTCTTT	813
Qy	661	 ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Db	814	 ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	873
Qy	721	 AAGCTCTGGGCCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGAGCGC	780
Db	874	 AAGCTCTGGGCCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGAGCGC	933
Qy	781	 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGG	840
Db	934	 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGG	993
Qy	841	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	 ATGGTGGTGCCTGGCTTCTGCCCTCTGCTACCTGCCATCAGCGCCTCAATGCTTT	960
Db	1054	 ATGGTGGTGCCTGGCTTCTGCCCTCTGCTACCTGCCATCAGCGCCTCAATGCTTT	1113
Qy	961	 AAGAGGGTGGATGTTCCGCCAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	1114	 AAGAGGGTGGATGTTCCGCCAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1173
Qy	1021	 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Db	1174	 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1233
Qy	1081	 CTCAGTGG 1088	
Db	1234	 CTCAGTGG 1241	

RESULT 7

US-08-846-704-1

; Sequence 1, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-846-704-1

Query Match 95.9%; Score 1086.4; DB 3; Length 1564;
Best Local Similarity 99.9%; Pred. No. 5.6e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db	154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db	214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 273
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db	274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
Qy	181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Db	334	CTGGTGGGCAACACGCTGGCTGCCTGGCGTGGCGAACACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	300
Db	394	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTCGGCCATGCCCTTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTCGGCCATGCCCTTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGG	633
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	634	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600.
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCATGGCCTATTCCAGATATTCCGC	720
Db	814	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCATGGCCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC	780
Db	874	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT	960
Db	1054	ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTGCGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1020
Db	1114	AAGAGGGTGTGCGGATGTTCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTTC	1173
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
		ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	

Db 1174 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCTCATCTACAACCTC 1233
Qy 1081 CTCAGTGG 1088
| | | | |
Db 1234 CTCAGTGG 1241

RESULT 8

US-08-846-704-3.

; Sequence 3, Application US/08846704
; Patent No. 6020157
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-846-704-3

Query Match 95.9%; Score 1086.4; DB 3; Length 1564;
Best Local Similarity 99.9%; Pred. No. 5.6e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGGCC 60

Db	154	ATGGAGCCCTAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC	333
Qy	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	334	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCATGCCCTTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	714	ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGCCAGATCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
|
Db 1054 ATGGTGGTGCTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCCTCAATGTCCTT 1113
Qy 961 AAGAGGGTGGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
|
Db 1114 AAGAGGGTGGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1173
Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
|
Db 1174 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233
Qy 1081 CTCAGTGG 1088
|
Db 1234 CTCAGTGG 1241

RESULT 9

US-08-462-509B-3

; Sequence 3, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1110 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1110
US-08-462-509B-3

Query Match 95.7%; Score 1084.8; DB 4; Length 1110;
Best Local Similarity 99.8%; Pred. No. 1.2e-249;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTCTG 120
Db 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360
Db 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480

Qy 481 GCCCGTGGCTCCATCTGGCATTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 540
Db 481 GCCCGTGGCTCCATCTGGCATTGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT 660
Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720

Db ||||||| 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Qy 721 AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC 780
Db ||||||| 721 AAGCTCTGGGGCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGGAACGGAAAGCGC 780
Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db ||||||| 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG 900
Db ||||||| 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG 900
Qy 901 ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
Db ||||||| 901 ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCGCTTC 1020
Db ||||||| 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCGCTTC 1020
Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
Db ||||||| 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
Qy 1081 CTCAGTGG 1088
Db ||||||| 1081 CTCAGTGG 1088

RESULT 10

PCT-US95-05616-1

; Sequence 1, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-1

Query Match 95.5%; Score 1081.6; DB 5; Length 1209;
Best Local Similarity 99.6%; Pred. No. 7.3e-249;
Matches 1084; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Db 61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGCTGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCCCAGCCTATGTGGCTGTGGCTGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTCAGTGGCCATGCCCTGTCAAG 360
Db 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTCAGTGGCCATGCCCTGTCAAG 360

Qy 361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 420
Db 361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600

Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCAGCTAGCCAACCGCACACGGCTTTCTCA 600
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660
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 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
 |||||
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
 Qy 721 AAGCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCGGAACGGAAAGCGC 780
 |||||
 Db 721 AACCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCGGAACGGAAAGCGC 780
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||
 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 |||||
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 Qy 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
 |||||
 Db 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
 |||||
 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020
 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 |||||
 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 Qy 1081 CTCAGTGG 1088
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 Db 1081 CTCAGTGG 1088

RESULT 11

PCT-US95-05616-3

; Sequence 3, Application PC/TUS9505616
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, ET AL.
 ; TITLE OF INVENTION: Human Neuropeptide Receptor
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1110 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-3

Query Match 95.0%; Score 1076.8; DB 5; Length 1110;
Best Local Similarity 99.4%; Pred. No. 1e-247;
Matches 1081; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
| |||||
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTCTG 120
| |||||
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
| |||||
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
| |||||
Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATGCCTG 300
| |||||
Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATGCCTG 300

Qy 301 CGGCCAGCCTGCTGGGACATCACTGAGTCCTGGCTGTCGGCATGCCCTGCAAG 360
| |||||
Db 301 CGGCCAGCCTGCTGGGACATCACTGAGTCCTGGCTGTCGGCATGCCCTGCAAG 360

Qy 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAATCTCAGCTTCATC 420
| |||||
Db 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAATCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGG 480
| |||||
Db 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGG 480

Qy	481	GCCCCGTGGCTCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCAGGCT	540
Db	481	GCCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	CTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Db	661	ATTGTACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAAGCTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT	960
Db	901	ATGGTGGTGTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGCTCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	961	AAGAGGGTGTGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGG 1088	
Db	1081	CTCAGTGG 1088	

RESULT 12

US-08-513-974B-375

; Sequence 375, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Hosoya, Masaki
 ; APPLICANT: Fujii, Ryo
 ; APPLICANT: Ohtaki, Tetsuya
 ; APPLICANT: Fukusumi, Shoji
 ; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 843 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..816
US-08-513-974B-375

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Query Match          61.6%;  Score 697.6;  DB 3;  Length 843;
Best Local Similarity  89.9%;  Pred. No. 2.4e-157;
Matches 748;  Conservative  0;  Mismatches  84;  Indels  0;  Gaps  0;

Qy          252 CATTGTCAACCTGTCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGGCCAGCCT 311
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          9 CGTGTTCATCCTGTCACTGGCCATGTGCTGGTACAGCCATCTGCCTGCCGGCCAGTCT 68

Qy          312 GCTGGTGGACATCACTGAGT CCTGGCTGTCGGCATGCCCTTGCAAGGT CATCCCCTA 371
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          69 GCTGGTAGACATCACGGAATCCTGGCTCTTGGCATGCCCTTGCAAGGT CATCCCCTA 128

Qy          372 TCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTATGCCCTGGACCG 431
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          129 TCTACAGGCCGTGTCCTGTCAGTGGCTGTGACTCTCAGCTCCATGCCCTGGACCG 188

Qy          432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGGCCGGCGGGCCCGTGGCTC 491
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACGTGCCGGCGGCCGCGCTC 248

Qy          492 CATCCTGGCATCTGGCTGTGTCGTGCCATCATGGTGCCCCAGGCTGCAGTCATGGA 551
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          249 CATCCTCGGCATCTGGCGGTGTCGTGCCATGGTGCTCATGGTGCTCAGGCTGCTGTGATGGA 308

Qy          552 ATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCAGTCTGTGATGA 611
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          309 GTGTAGCAGCGTGTGCCGAGCTGGCAACCGCACCCGCCTCTGTCTGTGATGA 368

Qy          612 ACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTA 671
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          369 GCGCTGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTATTGTCACCTA 428

Qy          672 CCTGGCCCCACTGGCCTCATGCCATGGCTATTCCAGATATTCCGCAAGCTGGGG 731
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          429 CCTGGCCCCACTGGCCTCATGCCATGGCTATTCCAGATCTCCGCAAGCTGGGG 488

Qy          732 CCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGGAAAGCGCCCTCAGACCA 791
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          489 CCGCCAGATCCCCGGCACCACTCGGCCCTGGTGCAGACTGGAAAGCGCCCTCAGACCA 548

Qy          792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCTTCCT 851
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCGCGCTTCCT 608

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Qy	852	GGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT	911
Db	609	GGCCGAGGTGAAACAGATGCGAGCCCGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT	668
Qy	912	GCTGGTCTCGCCCTCTGCTACCTGCCCATCAGCGCCTCAATGTCCTTAAGAGGGTGT	971
Db	669	GCTGGTCTCGCCCTCTGCTACCTGCCCATCAGTGCCTCAACGCTCAAGAGGGTCT	728
Qy	972	CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCGCTTCACCTCTCCA	1031
Db	729	CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCGCTTCACCTCTCCA	788
Qy	1032	CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTC	1083
Db	789	CTGGCTGGTGTACGCCAACAGCGCCGCCAACCTCCCTACTCCTCCTC	840

RESULT 13

US-08-513-974B-55

; Sequence 55, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Db	181	CCGCTGTTCAAGAGCACTGCCGGCGCCGCAGGCTCCATCCTCGGCATCTGGCG 240
Qy	511	GTGTCGCTGCCATCATGGGCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
Db	241	GTGTCGCTGGCTGTATGGGCCAGGCTGCTGTATGGAGTAGCAGCGTGCTGCC 300
Qy	571	GAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGCAGATGACCTC 630
Db	301	GAGCTGGCCAACCGCACCCGCCTCTGTCTGTGATGAGCGCTGGCAGACGACCTG 360
Qy	631	TATCCCAAGATCTACCACAGTTGCTCTTATTGTCACCTACCTGGCCCCACTGGCCTC 690
Db	361	TACCCCAAGATCTACCACAGCTGCTCTTCATTGTCACCTACCTGGCCCCACTGGCCTC 420
Qy	691	ATGGCCATGGCCTATTCCAGATATTCCGCAAGCTCTGGGCCAGATCCCCGGCACC 750
Db	421	ATGGCCATGGCCTATTCCAGATCTTCCGCAAGCTCTGGGCCAGATCCCCGGCACC 480
Qy	751	ACCTCAGCACTGGTGCAGAACTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAG 810
Db	481	ACCTCGGCCCTGGTGCAGAACTGGAAGCGCCCTCAGACCAGCTGGACGACCAGGGCAG 540
Qy	811	GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCGCCTCCTGGCTGAAGTGAAGCAGATG 870
Db	541	GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCGCCTCCTGGCGAGGTGAAACAGATG 600
Qy	871	CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGCTTCCCTCTGC 930
Db	601	CGAGCCCGAGGAAGACGGCAAGATGCTGATGGTGGTGTGCTGGTCTTCCCTCTGC 660
Qy	931	TACCTGCCCATCAGCGCCTCAATGCTTAAGAGGGTGTGCTGGATGTTCCGCAAGCC 990
Db	661	TACCTGCCCATCAGGCTCAACGCTCCTCAAGAGGGTCTCGGATGTTCCGCAAGCC 720
Qy	991	AGTGACCGCGAAGCTGTCTACGCCTGCTCACCTCTCCACTGGCTGGTGTACGCCAAC 1050
Db	721	AGCGACCGAGAGGCCATCTACGCCTGCTCACCTCTCCACTGGCTGGTGTACGCCAAC 780
Qy	1051	AGCGCTGCC 1059
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RESULT 14

US-09-461-436B-55

; Sequence 55, Application US/09461436B

; Patent No. 6538107

; GENERAL INFORMATION:

; APPLICANT: Shuji Hinuma

; Yasuaki Ito

; Ryo Fujii

; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwards & Angell, LLP

; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-461-436B-55

Query Match

59.2%; Score 670.6; DB 4; Length 789;

Best Local Similarity 90.6%; Pred. No. 6.5e-151;
Matches 715; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 271 GCTGACGTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
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Db 1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy 331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGGCTGTGTCCGTG 390
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TCCTGGCTCTTGGCATGCCCTCTGCAAGGTATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy 391 TCAGTGGCAGTGCTAATCTCAGCTTCATGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TCAGTGGTCGTGCTGACTCTCAGCTCCATGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy 451 CCACTATTGTTCAAGAGCACAGCCGGCGGGCCCGTGGCTCCATCCTGGCATCTGGGCT 510
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CCGCTGTTGTTCAAGAGCACTGCCGGCGCGCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy 511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
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Db 241 GTGTCGCTGGCTGTCATGGTGCCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGTGCC 300

Qy 571 GAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGCAGATGACCTC 630
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GAGCTGGCCAACCGCACCCGCCCTCCTGTCTGTGATGAGCGCTGGCAGACGACCTG 360

Qy 631 TATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCCCACTGGCCTC 690
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TACCCAAGATCTACCACAGCTGCTTCTTATTGTCACCTACCTGGCCCCACTGGCCTC 420

Qy 691 ATGGCCATGGCTATTCCAGATATTCCGCAAGCTCTGGGCCAGATCCCCGGCACC 750
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ATGGCCATGGCTATTCCAGATCTCCGCAAGCTCTGGGCCAGATCCCCGGCACC 480

Qy 751 ACCTCAGCACTGGTGGGAACCTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAG 810
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ACCTCGGCCCTGGTGCCTGCAACTGGAAGCGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy 811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCGCCTCCTGGCTGAAGTGAAGCAGATG 870
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCGCCTCCTGGCGAGGTGAAACAGATG 600

Qy 871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC 930
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Db 601 CGAGCCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC 660

Qy 931 TACCTGCCCATCAGCGCCTCAATGCTTAAGAGGGTGTTCGGATGTTCCGCCAAGCC 990
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 TACCTGCCCATCAGTGCCTCAAGCCTCAAGAGGGTCTTCGGATGTTCCGCCAAGCC 720

Qy 991 AGTGACCGCGAAGCTGTCTACGCCCTGCTCACCTCTCCACTGGCTGGTGTACGCCAAC 1050
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Db 721 AGCGACCGAGAGGCCATCTACGCCCTGCTCACCTCTCCACTGGCTGGTGTACGCCAAC 780

Qy 1051 AGCGCTGCC 1059
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Db 781 AGCGCCGCC 789

RESULT 15
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; Sequence 1, Application US/09119788
; Patent No. 6166193
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,788
; FILING DATE: 21-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-119-788-1

Query Match 46.0%; Score 520.8; DB 3; Length 1633;
Best Local Similarity 70.5%; Pred. No. 4.2e-115;
Matches 712; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

Qy 80 ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db 217 ACGACGAGGAATTCTGCAGGTACCTGTGGAGGGAAACCTGCACCCGAAAGAATATGAGT 276

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCCCTGGTGGCAACACGCTGG 199

Db	277	GGTCCTGATGCCGGTACATCATCGTGTGCTGGCTCTCATTGGAACGTCTGG	336
Qy	200	TCTGCCTGGCGTGTGGCGAACCAACCACATGAGGACAGTCACCAACTACTCATTGTCA	259
Db	337	TTTGTGTGGCAGTGTGGAAGAACCAACCACATGAGGACGGTAACCAACTACTCATAGTCA	396
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGCCAGCCTGCTGGTGG	319
Db	397	ATCTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCCTCAGCCACACTGGTCGTGG	456
Qy	320	ACATCACTGAGTCCTGGCTGTCGGCCATGCCCTTGCAAGGTACATCCCCTATCTACAGG	379
Db	457	ATATCACTGAGACCTGGTTTTGGACAGTCCTTGCAAAGTGATTCCCTATCTACAGA	516
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGTATG	439
Db	517	CCGTGTGGTGTCTGTGCTGCTCACACTGAGCTGATGCCCTGGATCGGTGGTATG	576
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGGGCCGTGGCTCCATCCTGG	499
Db	577	CAATCTGTCACCCTTGATGTTAAGAGCACAGCAAAGCGGGCCGTAACAGCATTGTCA	636
Qy	500	GCATCTGGGCTGTGTCGCTGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	637	TCATCTGGATTGTCCTGCATTATAATGATTCCCTAGGCCATCGTCATGGAGTGCAGCA	696
Qy	560	GTGTGCTGCCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGG	619
Db	697	CCGTGTCCTCAGGCTTAGCCAATAAACCCACCCCTTTACGGTGTGTGATGAGCGCTGGG	756
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGCC	679
Db	757	GTGGTAAAATTATCCAAGATGTACCATCTGTTCTTCTGGTACATACATGGCAC	816
Qy	680	CACTGGCCTCATGCCATGCCATTTCAGATATTCCGCAAGCTCTGGGCCAGA	739
Db	817	CACTGTGTCATGGTGTGCTTATCTGCAAATATTGCAAACTCTGGTGTGACAGA	876
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCAGAACGGAAAGCGCCCTCAGACCAGCTGGGG	799
Db	877	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTT	930
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCGCTTCTGGCTGAAG	859
Db	931	CACAGCCTCGAGGGCAGGACAGCCAACGAAGTCCGGATGGCGCTGTGGCGGTGAAA	990
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCT	919
Db	991	TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCGGATGTTGATGGTGTGCTTTGGTAT	1050
Qy	920	TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTTAAGAGGGTGTGGATGT	979
Db	1051	TTGCAATTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTGGGATGT	1110
Qy	980	TCCGCCAAGCCAGTGACCGCGAACGCTGTCTACGCCCTGCTCACCTCTCCACTGGCTGG	1039

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Qy 1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGA 1089
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Search completed: October 15, 2004, 22:55:10

Job time : 90.8123 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 584.359 Seconds
(without alignments)
9829.265 Million cell updates/sec

Title: US-10-070-532-5

Perfect score: 1133

Sequence: 1 atggagccctcagccacccc.....tcctgaccatcggtccccgg 1133

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result

Query

No.	Score	Match Length	DB	ID	Description
1	1131.4	99.9	1133	10 US-09-393-696-5	Sequence 5, Appli
2	1114.4	98.4	1116	14 US-10-077-874-5	Sequence 5, Appli
3	1086.4	95.9	1564	15 US-10-225-567A-367	Sequence 367, App
4	1086.4	95.9	1564	16 US-10-352-684A-21	Sequence 21, Appl
5	1084.8	95.7	1110	14 US-10-077-874-3	Sequence 3, Appli
6	1084.8	95.7	1209	14 US-10-077-874-1	Sequence 1, Appli
7	1084.8	95.7	1564	9 US-09-828-538-23	Sequence 23, Appl
8	1081.6	95.5	1209	10 US-09-393-696-1	Sequence 1, Appli
9	1081.6	95.5	1278	11 US-09-826-509-548	Sequence 548, App
10	1076.8	95.0	1110	10 US-09-393-696-3	Sequence 3, Appli
11	912	80.5	1281	9 US-09-730-931-1	Sequence 1, Appli
12	670.6	59.2	789	15 US-10-278-087A-55	Sequence 55, Appl
13	520.8	46.0	1633	15 US-10-282-717-1	Sequence 1, Appli
14	520.8	46.0	1843	15 US-10-225-567A-369	Sequence 369, App
15	516	45.5	1335	11 US-09-826-509-550	Sequence 550, App
16	249.2	22.0	9785	9 US-09-961-848-1	Sequence 1, Appli
17	249.2	22.0	10453	9 US-09-828-538-21	Sequence 21, Appl
18	244	21.5	244	9 US-09-828-538-6	Sequence 6, Appli
19	225.4	19.9	227	9 US-09-828-538-10	Sequence 10, Appli
20	197.4	17.4	356	9 US-09-828-538-2	Sequence 2, Appli
21	179	15.8	179	9 US-09-828-538-4	Sequence 4, Appli
22	163.2	14.4	1290	17 US-10-719-587-55	Sequence 55, Appl
23	163.2	14.4	1290	17 US-10-719-587-56	Sequence 56, Appl
24	163.2	14.4	1293	9 US-09-866-248A-7	Sequence 7, Appli
25	163.2	14.4	1293	15 US-10-225-567A-657	Sequence 657, App
26	163.2	14.4	1320	9 US-09-292-973-3	Sequence 3, Appli
27	156.2	13.8	1299	17 US-10-719-587-38	Sequence 38, Appl
28	156.2	13.8	1410	9 US-09-866-248A-1	Sequence 1, Appli
29	149.8	13.2	1532	9 US-09-292-973-1	Sequence 1, Appli
30	128.4	11.3	168575	15 US-10-178-194-1	Sequence 1, Appli
31	124.4	11.0	977	12 US-09-876-143-1561	Sequence 1561, Ap
32	122	10.8	122	9 US-09-828-538-12	Sequence 12, Appl
33	120.6	10.6	1174	17 US-10-611-210-9	Sequence 9, Appli
34	119.8	10.6	1174	17 US-10-611-210-7	Sequence 7, Appli
35	119	10.5	1110	14 US-10-044-592-17	Sequence 17, Appl
36	119	10.5	1110	15 US-10-278-087A-31	Sequence 31, Appl
37	119	10.5	1113	15 US-10-225-567A-244	Sequence 244, App
38	119	10.5	1152	17 US-10-611-210-10	Sequence 10, Appl
39	119	10.5	1331	14 US-10-044-592-73	Sequence 73, Appl
40	118.4	10.5	1173	17 US-10-611-210-6	Sequence 6, Appli
41	116	10.2	116	9 US-09-828-538-8	Sequence 8, Appli
42	115.8	10.2	1174	17 US-10-611-210-8	Sequence 8, Appli
43	107.2	9.5	669	14 US-10-044-592-70	Sequence 70, Appli
c 44	105.6	9.3	436	13 US-10-027-632-275272	Sequence 275272,
c 45	105.6	9.3	436	16 US-10-027-632-275272	Sequence 275272,

ALIGNMENTS

RESULT 1

US-09-393-696-5

; Sequence 5, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1131)
US-09-393-696-5

Query Match 99.9%; Score 1131.4; DB 10; Length 1133;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTATCTG 120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 180
Qy	181 CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Db	181 CTGGTGGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Qy	301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
Db	301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
Qy	361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db	361 GTCATCCCCATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGGG 480
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGCGCTGGCCATCATGGTCCCCAGGGCT 540

Db ||||||| 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGCCATCATGGTCCCCAGGCT 540

Qy ||||||| 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA 600

Db ||||||| 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCA 600

Qy ||||||| 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660

Db ||||||| 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660

Qy ||||||| 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCAGATATTCCGC 720

Db ||||||| 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCAGATATTCCGC 720

Qy ||||||| 721 AAGCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC 780

Db ||||||| 721 AAGCTCTGGGGCCGCAGATCCCCGGCACCAACCTCAGCACTGGTGGAACTGGAAGCGC 780

Qy ||||||| 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840

Db ||||||| 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840

Qy ||||||| 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Db ||||||| 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy ||||||| 901 ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960

Db ||||||| 901 ATGGTGGTGTGCTGGTCTTCGCCCTTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960

Qy ||||||| 961 AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020

Db ||||||| 961 AAGAGGGTGGTGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020

Qy ||||||| 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080

Db ||||||| 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC 1080

Qy ||||||| 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCCTGACCATCGTGCCCCGG 1133

Db ||||||| 1081 CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCCCTGACCATCGTGCCCCGG 1133

RESULT 2

US-10-077-874-5

; Sequence 5, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

;
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/077,874
; FILING DATE: 20-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,509
; FILING DATE: 05-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1116
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-077-874-5

Query Match 98.4%; Score 1114.4; DB 14; Length 1116;
Best Local Similarity 99.9%; Pred. No. 6.2e-311;
Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC	60
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Qy	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300

Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCCATGCCCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGCCCATGCCCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG	480
Db	421	GCCCTGGACCCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG	480
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Qy	601	GTCTGTGATGAAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCATGGCTATTCCAGATAATTCCGC	720
Db	661	ATTGTACACTACCTGGCCCCACTGGGCCTCATGGCATGGCTATTCCAGATAATTCCGC	720
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGCG	780
Db	721	AAGCTCTGGGCCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGCG	780
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCTCTCAATGTCTT	960
Db	901	ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCTCTCAATGTCTT	960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCGTCTTC	1020
Db	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCGTCTTC	1020
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Db	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Qy	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCC	1116
Db	1081	CTCAGTGGATGTAAGAGAAGAGTCTAGTTCTGTCC	1116

RESULT 3

US-10-225-567A-367

; Sequence 367, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 367

; LENGTH: 1564

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-367

Query Match 95.9%; Score 1086.4; DB 15; Length 1564;
Best Local Similarity 99.9%; Pred. No. 8e-303;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 273

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
|||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 274 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACATGAGGACAGTC 240
|||||||||||||||||||||||||||||||||||||||||||||||||||

Db 334 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGGAACCACATGAGGACAGTC 393

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
|||||||||||||||||||||||||||||||||||||||||||||||||||

Db 394 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453

Qy 301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
|||||||||||||||||||||||||||||||||||||||||||||||

Db 454 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 513

Qy 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
|||||||||||||||||||||||||||||||||||||||||||

Db 514 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCAGCGG	633
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	540
Db	634	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCAGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCAGATCCCCGGCACCACTCAGCACTGGTGCAGACTGGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTC	1020
Db	1114	AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTC	1173
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1080
Db	1174	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCACCCATCATCTACAACCTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 4

US-10-352-684A-21

; Sequence 21, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen

; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1431)
US-10-352-684A-21

Query Match 95.9%; Score 1086.4; DB 16; Length 1564;
Best Local Similarity 99.9%; Fred. No. 8e-303;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db	154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213
Qy	61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Db	214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTG 273
Qy	121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 180

Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTCGTGGCC 333
Qy	181	CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db	334	CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 393
Qy	241	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db	394	ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG 633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTCTCA 753
Qy	601	GTCTGTGATGAAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db	754	GTCTGTGATGAAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 873
Qy	721	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCG 780
Db	874	AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGCG 933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGCAGAGCCCCAGCCCCGGGC 993
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db	994	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy	901	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCTT 960
Db	1054	ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCTT 1113
Qy	961	AAGAGGGTGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC 1020

Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
Qy 1021 ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
|
Db 1174 ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233
Qy 1081 CTCAGTGG 1088
|
Db 1234 CTCAGTGG 1241

RESULT 5

US-10-077-874-3

; Sequence 3, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1110 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1110

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-077-874-3

Query Match 95.7%; Score 1084.8; DB 14; Length 1110;
Best Local Similarity 99.8%; Pred. No. 2.1e-302;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTATTCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360
Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAAGACTCTCAGCTTCATC 420
Db 361 GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGCTAAGACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480

Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC 780
Db 721 AAGCTCTGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCAGAACGGC 780

Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGT GCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 901 ATGGTGGT GCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 961 AAGAGGGTGTTCGGGATGTTCCGCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080

Qy 1081 CTCAGTGG 1088
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Db 1081 CTCAGTGG 1088

RESULT 6

US-10-077-874-1

; Sequence 1, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1209
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-874-1

Query Match 95.7%; Score 1084.8; DB 14; Length 1209;
Best Local Similarity 99.8%; Pred. No. 2.2e-302;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Db	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG	120
Qy	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGCTCGTGGCC	180
Db	121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGGCTCGTGGCC	180
Qy	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Db	181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC	240
Qy	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Qy	301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Db	301 CGGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Qy	361 GTCATCCCTATCTACAGGCTGTGTCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361 GTCATCCCTATCTACAGGCTGTGTCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Qy	481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	540
Db	481 GCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGTGGCCATCATGGTCCCCAGGCT	540
Qy	541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600

Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCAGCTAGCCAACCGCACACGGCTTTCTCA 600
 Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660
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 Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAAGATCTACCACAGTTGCTTCTT 660
 Qy 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCCAGATATTCCGC 720
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 Db 661 ATTGTACCTACCTGGCCCCACTGGCCTCATGGCCATGGCTATTCCAGATATTCCGC 720
 Qy 721 AAGCTCTGGGCCCGCAGATCCCCGGCACACCTCAGCACTGGTGCAGAAGCTGGAAGCGC 780
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 Db 721 AAGCTCTGGGCCCGCAGATCCCCGGCACACCTCAGCACTGGTGCAGAAGCTGGAAGCGC 780
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||||
 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 Qy 841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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 Db 841 CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 Qy 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
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 Db 901 ATGGTGGTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
 Qy 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
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 Db 1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 Qy 1081 CTCAGTGG 1088
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 Db 1081 CTCAGTGG 1088

RESULT 7

US-09-828-538-23

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; Sequence 23, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726

```

; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-828-538-23

Query Match 95.7%; Score 1084.8; DB 9; Length 1564;
 Best Local Similarity 99.8%; Pred. No. 2.3e-302;
 Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGTGTATTCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCGCTATCTGTGGCGCGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333
Qy	181	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	240
Db	334	CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGTAACCTCAGCTTCATC	420
Db	514	GTCATCCCTATCTACAGGCTGTGTCAGTGGCAGTGTAACCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG	633
Qy	481	GCCCCTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGTAACCTCAGCTTCATC	540
Db	634	GCCCCTGGCTCCATCCTGGCATCTGGCTGTGTCAGTGGCAGTGTAACCTCAGCTTCATC	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGAGCTAGCCAACCGCACACGGCTTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGAGCTAGCCAACCGCACACGGCTTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGCAGATGACCTATCCAAAGATCTACCACAGTTGCTTCTT	660

Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAAGCTGGAGCGC	780
Db	874	AAGCTCTGGGGCGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAAGCTGGAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	840
Db	934	CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGTGCTGGCTTCCGCCCCCTGCTACCTGCCATCAGCGTCTCAATGTCCTT	960
Db	1054	ATGGTGGTGTGCTGGCTTCCGCCCCCTGCTACCTGCCATCAGCGTCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGGTTCGGGATGTTCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGGTTCGGGATGTTCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG 1088	
Db	1234	CTCAGTGG 1241	

RESULT 8

US-09-393-696-1

; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)..(1209)
US-09-393-696-1

Query Match 95.5%; Score 1081.6; DB 10; Length 1209;
Best Local Similarity 99.6%; Pred. No. 1.8e-301;
Matches 1084; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120
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Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
|||
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCCAGCCTATGTGGCTGTGTTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240
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Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGGAACCACCATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
|||
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTGCAAG 360
|||
Db 301 CCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
|||
Db 361 GTCATCCCCTATCTACAGGCTGTGTCCTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480
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Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCG 480

Qy 481 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
|||
Db 481 GCCCGTGGCTCCATCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
|||
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
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Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
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Db 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGCCAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGC 780
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Db 721 AACCTCTGGGGCCGCCAGATCCCCGGCACCAACCTCAGCACTGGTGCAGAACCTGGAAGCGC 780
 Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 |||||||
 Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGC 840
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 |||||||
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
 Qy 901 ATGGTGTTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
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 Db 901 ATGGTGTTGCTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
 Qy 961 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCCTGCTTC 1020
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 Db 961 AAGAGGGTGGTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCCTGCTTC 1020
 Qy 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
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 Db 1021 ACCTTCTCCCCTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC 1080
 Qy 1081 CTCAGTGG 1088
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 Db 1081 CTCAGTGG 1088

RESULT '9

US-09-826-509-548

; Sequence 548, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 548

; LENGTH: 1278

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-548

Query Match 95.5%; Score 1081.6; DB 11; Length 1278;

Best Local Similarity 99.6%; Pred. No. 1.8e-301;

Matches 1084; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGTCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTG 300

Qy 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360
Db 301 CGGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCGTGCACTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCCTATCTACAGGCTGTGTCGTGCACTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGGG 480

Qy 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGCATCTGGCTGTGTCGCTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTA 600

Qy 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTGCTTCTT 660
Db 601 GTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTGCTTCTT 660

Qy 661 ATTGTACACTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720
Db 661 ATTGTACACTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCAGAACCTGGAGCGC 780
Db 721 AAGCTCTGGGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCAGAACCTGGAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Db	841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAGATGCTG	900
Qy	901 ATGGTGGTGCCTGGCTGGCTCTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Db	901 ATGGTGGTGCCTGGCTCTCGCCCTCTGCTACCTGCCATCAGCGCCTCAATGTCCTT	960
Qy	961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961 AAGAGGGTGGTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC	1080
Db	1021 ACCTTCTCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTC	1080
Qy	1081 CTCAGTGG 1088	
Db	1081 CTCAGTGG 1088	

RESULT 10

US-09-393-696-3

; Sequence 3, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1110)

US-09-393-696-3

Query Match 95.0%; Score 1076.8; DB 10; Length 1110;
Best Local Similarity 99.4%; Pred. No. 4.3e-300;
Matches 1081; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120
Db	61 TCCCCCTGTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTG	120

Qy 121 TACCCAAAACAGTATGAGTGGGCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGGCCTCATCGCAGCCTATGTGGCTGTTCGTCGTGGCC 180

Qy 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240
Db 181 CTGGTGGCAACACGCTGGCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 300
Db 241 ACCAACTACTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGAUTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGGCCATGCCCTTGCAAG 360
Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGGCCATGCCCTTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGG 480
Db 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600
Db 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660
Db 601 CTCTGTGATGAACGCTGGGAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720
Db 661 ATTGTCACCTACCTGGCCCCACTGGCCTCATGGCCATGGCCTATTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGCCGAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGCAGCGC 780
Db 721 AAGCTCTGGGCCGAGATCCCCGGCACACCTCAGCACTGGTGCAGAACGGCAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840
Db 781 CCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGC 840

Qy 841 CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 841 CGCGCCTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960
Db 901 ATGGTGGTGTGCTGGCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTACGCCGTGCTTC 1020

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Db          ||||||| 961 AAGAGGGTGGATGTCGGCAAGCCAGTGACCGCGAAGCTGTACGCCCTGCTTC 1020
Qy          1021 ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
Db          1021 ACCTTCTCCC ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
Qy          1081 CTCAGTGG 1088
Db          1081 CTCAGTGG 1088

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RESULT 11

US-09-730-931-1

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; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: DOG OREXIN 1 RECEPTOR
; FILE REFERENCE: GH-70669
; CURRENT APPLICATION NUMBER: US/09/730,931
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,373
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

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Query Match      80.5%; Score 912; DB 9; Length 1281;
Best Local Similarity 90.3%; Pred. No. 1.5e-252;
Matches 988; Conservative 0; Mismatches 100; Indels 6; Gaps 1;

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Qy          1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
Db          1 ATGGAGCCCTCAGCCACCCAGGGGCCAGACTGGGACCCCCACGGCGGGAGCTG 60
Qy          61 TCCCCT-----GTGCCTCCAGACTATGAAGATGAGTTCTCCGCTATCTGTGGCGTGAT 114
Db          61 TCTCCGTCACTGGTGCCTCCGACTATGAAGACGAGTTCCCTGCCTATCTGTGGCGCAT 120
Qy          115 TATCTGTACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCGTC 174
Db          121 TACCTGTACCCAAAGCAGTATGAGTGGGTCTCATCGCTGCCTACGTGGCTGTGTTCTA 180
Qy          175 GTGGCCCTGGTGGCAACACGCTGGTCTGCCGTGTGGCGAACACCACATGAGG 234
Db          181 GTGGCCCTGGTGGCAACACGCTGGTCTGCCGTGTGGAGGAACCACCATGAGG 240
Qy          235 ACAGTCACCAACTACTTCATTGTCAACCTGTCCTGGCTGACGTTCTGGTGACTGCTATC 294
Db          241 ACGGTACCAACTATTCATTGTCAACCTGTCCTGGCTGATGTGCTGGTACAGCCATC 300
Qy          295 TGCCTGCCGGCCAGCCTGCTGGTGACATCACTGAGTCCTGGCTGTTGGCCATGCCCTC 354

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Db	301	TGCCTCCGGCCAGCCTGCTGGTAGACATCACTGAGTCCTGGCTTCGGTCATAACCCTC	360
Qy	355	TGCAAGGTATCCCCTATCTACAGGCTGTGCCGTGTCAGTGGCAGTGCTAACTCTCAGC	414
Db	361	TGCAAAGTCATCCCCTACCTACAGGCCGTGTCGGTGGCAGTGCTGACTCTCAGC	420
Qy	415	TTCATGCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCC	474
Db	421	TTCATGCCCTGGACCGCTGGTATGCCATCTGCCACCCGCTGTTCAAGAGCACCGCC	480
Qy	475	CGGCGGGCCCGTGGCTCCATCCTGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGC	534
Db	481	CGGCGCGCCCGCAGCTCCATCCTGGCATCTGGGCTGTGTCATTGGCTGTCAAGAGCACCGCC	540
Qy	535	CAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCAGGCTAGCCAACCGCACACGGCTC	594
Db	541	CAGGCTGCCGTATGGAATGCAGCAGCGTGTCCCTGAGCTAGCCAACCGCACCGCCTC	600
Qy	595	TTCTCAGTCTGTGATGAACGCTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGC	654
Db	601	TTCTCTGTGATGAACACTGGCAGATGACCTCTATCCAAGATCTACCACAGTTGC	660
Qy	655	TTCTTTATGTACCTACCTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATA	714
Db	661	TTCTTCATTGTCACCTACTGGCCCCACTGGCCTCATGGCATGGCTATTCCAGATC	720
Qy	715	TTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGC	774
Db	721	TTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGCACCACTGGCCCTGGTGAGGA	780
Qy	775	AAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCC	834
Db	781	AAGCGCCCTCGGACCAGCTGGAGGACCAGGGGCCCTGAGCGCGAACCCCCCCT	840
Qy	835	CGGGGCCGCGCTTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAG	894
Db	841	CGGGCCCGGGCTTCTGGCTGAGGTGAAGCAGATGCGAGCGCGAGGAAGACGGCCAAG	900
Qy	895	ATGCTGATGGTGGTCTGCTGGCTTCGCCCTTGCTACCTGCCATCAGCGTCTCAAT	954
Db	901	ATGCTGATGGTCTGCTGGCTTGCCCTTGCTACCTGCCATCAGTGTCTCAAT	960
Qy	955	GTCCTTAAGAGGGTGTTCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC	1014
Db	961	GTCCTCAAGAGGGTGTTCGGATGTTCCGCCAATCCAGTGACCGAGAAGCCGTACGCC	1020
Qy	1015	TGCTTCACCTCTCCACTGGCTGGTACGCCAACAGCGTGCACCCATCATCTAC	1074
Db	1021	TGCTTCACCTCTCCACTGGCTGGTATGCCAACAGCGTGCACCCATCATCTAC	1080
Qy	1075	AACTTCCTCAGTGG 1088	
Db	1081	AACTTCCTCAGCGG 1094	

US-10-278-087A-55

; Sequence 55, Application US/10278087A
; Publication No. US20030138817A1

; GENERAL INFORMATION:

; APPLICANT: Shuji Hinuma
; Yasuaki Ito
; Ryo Fujii

; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwards & Angell, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0; Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/278,087A
; FILING DATE: 31-Jan-2003
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/461,436
; FILING DATE: 14-DEC-1999
; APPLICATION NUMBER: 09/038,572
; FILING DATE: 11-MAR-1998
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, DAVID G.

; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-278-087A-55

Query Match 59.2%; Score 670.6; DB 15; Length 789;
Best Local Similarity 90.6%; Pred. No. 5.4e-183;
Matches 715; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy 331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGGCTGTGTCCGTG 390
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TCCTGGCTTTGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy 391 TCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TCAGTGGTCGTGCTGACTCTCAGCTCCATGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy 451 CCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCCTGGCATCTGGGCT 510
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CCGCTGTTGTTCAAGAGCACTGCCCGCGCCCGCGGCTCCATCCTGGCATCTGGGCG 240

Qy 511 GTGTCGCTGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCC 300

Qy 571 GAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGCAGATGACCTC 630
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GAGCTGGCCAACCGCACCCGCCCTCTGTCTGTGATGAGCGCTGGCAGACGACCTG 360

Qy 631 TATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCCCACTGGGCTC 690
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCTC 420

Qy 691 ATGGCCATGGCCTATTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ATGGCCATGGCCTATTCCAGATCTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy 751 ACCTCAGCACTGGTGCAGGAACCTGGAAGCGCCCTCAGACCAGCTGGGGACCTGGAGCAG 810
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ACCTCGGCCCTGGTGCAGCACTGGAAGCGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy 811 GGCGCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTCCTGGCTGAAGTGAAGCAGATG 870
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCCCTCCTGGCCGAGGTGAAACAGATG 600
 Qy 871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGCTTCGCCCTCTGC 930
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 601 CGAGCCCGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGCTTCGCCCTCTGC 660
 Qy 931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 661 TACCTGCCCATCAGTGTCCCTAACGTCCCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720
 Qy 991 AGTGACCGCGAAGCTGTCTACGCCCTGCTCACCTTCTCCCACGGCTGGTGACGCCAAC 1050
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 721 AGCGACCGAGAGGCCATCTACGCCCTGCTCACCTTCTCCCACGGCTGGTGACGCCAAC 780
 Qy 1051 AGCGCTGCC 1059
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 Db 781 AGCGCCGCC 789

RESULT 13

US-10-282-717-1

; Sequence 1, Application US/10282717
 ; Publication No. US20030083466A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YANAGISAWA, MASASHI
 ; TITLE OF INVENTION: cDNA CLONE MY1 THAT ENCODES A NOVEL
 ; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
 ; FILE REFERENCE: GH50029D1C1
 ; CURRENT APPLICATION NUMBER: US/10/282,717
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/676,625
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 09/119,788
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: 60/053,790
 ; PRIOR FILING DATE: 1997-07-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1633
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS

US-10-282-717-1

Query Match 46.0%; Score 520.8; DB 15; Length 1633;
 Best Local Similarity 70.5%; Pred. №. 1e-139;
 Matches 712; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

Qy 80 ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 217 ACGACGAGGAATTCCCTGCGGTACCTGTGGAGGAAATACCTGCACCCGAAAGAATATGAGT 276

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTCGTGGCCCTGGTGGCAACACGCTGG 199
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 277 GGGTCCTGATGCCGGTACATCATCGTGGCTCTCATTGGAACGTCCTGG 336

Qy 200 TCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTCATTGTCA 259

Db	337	TTTGTGTGGCAGTGTGGAAGAACCAACCATGAGGACGGAACCTACTTCATAGTCA	396
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGGCAGCCTGCTGGTGG	319
Db	397	ATCTTCTCTGGCTGATGTGCTCGTACCATCACCTGCCTCCAGCCACACTGGTCGTGG	456
Qy	320	ACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGG	379
Db	457	ATATCACTGAGACCTGGTTTTGGACAGTCCCTTGCAAAGTGATTCCCTATCTACAGA	516
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCCTGGTATG	439
Db	517	CCGTGTCGGTGTCTGTCCTCACACTGAGCTGTATGCCCTGGATCGGTGGTATG	576
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGGGCCGTGGCTCCATCCTGG	499
Db	577	CAATCTGTCACCCCTTGATGTTAAGAGCACAGCAAAGCGGGCCGTAACAGCATTGTCA	636
Qy	500	GCATCTGGGCTGTGTCGCTGGCCATCATGGTCCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	637	TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA	696
Qy	560	GTGTGCTGCCGTGAGCTAGCCAACCGCACACGGCTCTTCAGTCTGTGATGAAACGCTGGG	619
Db	697	CCGTGTTCCCAGGCTAGCCAATAAAACCACCCCTTTACGGTGTGATGAGCGCTGGG	756
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	757	GTTGGAAATTATCCAAGATGTACCAACATCTGTTCTTCTGGTGACATACATGGCAC	816
Qy	680	CACTGGGCCTCATGGCATGGCTATTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA	739
Db	817	CACTGTGTCATGGTGTGGCTATCTGCAAATATTGCAAACACTGGTGTGACAGA	876
Qy	740	TCCCCGGCACCCACTCAGCACTGGTGCAGAACCTGGAAAGCGCCCTCAGACCAGCTGGGG	799
Db	877	TCCCTGGAACATCATCTGTAGTTAGAGAAAATGGAAGCCCC-----TGCAGCCTGTT	930
Qy	800	ACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGGCGCGCCTCTGGCTGAAG	859
Db	931	CACAGCCTCGAGGGCAGGACAGCCAACGAAGTCCGGATGGCGCTGTGGCGCTGAAA	990
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCT	919
Db	931	TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCGGATGTTGATGGTGTGCTTGGTAT	1050
Qy	920	TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTTAAGAGGGTGTGGGATGT	979
Db	1051	TTGCAATTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTGGGATGT	1110
Qy	980	TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTCACCTTCTCCACTGGCTGG	1039
Db	1111	TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCCTGGTTACCTTTCACACTGGCTTG	1170
Qy	1040	TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGAA	1089

Db 1171 TATATGCCAATAGTGCCTCGAACATTATAATTTCAGTGGA 1220

RESULT 14

US-10-225-567A-369

; Sequence 369, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 369

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-369

Query Match 46.0%; Score 520.8; DB 15; Length 1843;
Best Local Similarity 70.5%; Pred. No. 1e-139;
Matches 712; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

Qy 80 ATGAAGATGAGTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
| || || || || || || || || || || || || || || || || || || || || || || ||

Db 428 ACGACGAGGAATTCCCTGCGGTACCTGTGGAGGAAATACCTGCACCCGAAAGAATATGAGT 487

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTCGTCGGCCCTGGTGGGCAACACGCTGG 199
| || || || || || || || || || || || || || || || || || || || || || || ||

Db 488 GGGTCCTGATGCCGGGTACATCATCGTGTGTCGTGGCTCTCATGGAACGTCCTGG 547

Qy 200 TCTGCCTGGCGTGTGGCGAACACCACATGAGGACAGTCACCAAACACTTCATTGTCA 259
| || || || || || || || || || || || || || || || || || || || || || ||

Db 548 TTTGTGTGGCAGTGTGGAAGAACCAACATGAGGACGGTAACCAAACACTTCATAGTCA 607

Qy 260 ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGCCAGCCTGCTGGTGG 319
| || || || || || || || || || || || || || || || || || || || || || ||

Db 608 ATCTTTCTGGCTGATGTGTCGTGACCATCACCTGCCCTCAGGCCACACTGGTCGTGG 667

Qy 320 ACATCACTGAGTCCTGGCTGTTGGCCATGCCCTCTGCAAGGTACATCCCCTATCACAGG 379
| || || || || || || || || || || || || || || || || || || || || || ||

Db 668 ATATCACTGAGACCTGGTTTTGGACAGTCCCTTGCAAAAGTGATTCCCTATCTACAGA 727

Qy 380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGTATG 439
| || || || || || || || || || || || || || || || || || || || || || ||

Db 728 CCGTGTGGTGTCTGTGTCCTCACACTGAGCTGATGCCCTGGATGGTGGTATG 787

Qy 440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGGGCCCGTGGCTCCATCCTGG 499
| || || || || || || || || || || || || || || || || || || || || || |

Db	788	CAATCTGTCACCCTTGATGTTAACAGCACAGCAAAGCGGGCCGTAACAGCATTGTCA	847
Qy	500	GCATCTGGGCTGTGTCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	848	TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTAGGCCATCGTCATGGAGTGCAGCA	907
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGG	619
Db	908	CCGTGTTCCCAGGCTTAGCCAATAAACACCCTCTTACGGTGTGTGATGAGCGCTGGG	967
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	968	GTGGTGAATTATCCAAGATGTACCATCTGTTCTTCTGGTGACATACATGGCAC	1027
Qy	680	CACTGGGCCTCATGGCATGGCCTATTCAGATATTCCGCAAGCTCTGGGCCGAGA	739
Db	1028	CACTGTGTCATGGTGTGGCTTATCTGCAAATATTGCAAACTCTGGTGTGACAGA	1087
Qy	740	TCCCCGGCACCACTCAGCACTGGTGGAACTGGAAGGCCCTCAGACCAGCTGGGG	799
Db	1088	TCCCTGGAACATCATCTGTAGTTAGAGAAAATGGAAGCCCC-----TGCAGCCTGTT	1141
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGGCCAGCCCCGGGCGCCTCCTGGCTGAAG	859
Db	1142	CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCGGATGAGCGCTGGCGGCTGAAA	1201
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCT	919
Db	1202	TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCGGATGTTGATGGTTGTGCTTTGGTAT	1261
Qy	920	TCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTAACAGGGTGGCTGGATGT	979
Db	1262	TTGCAATTGCTATCTACCAATTAGCATCCTCAATGTGCTAACAGAGAGTATTGGATGT	1321
Qy	980	TCCGCCAAGCCAGTGACCGCGAACGCTGCTACGCCGCTTACCTCTCCACTGGCTGG	1039
Db	1322	TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCGGTTACCTTTACACTGGCTTG	1381
Qy	1040	TGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTCAGTGGAA	1089
Db	1382	TATATGCCAACAGAGACTGTGTATGCCGGTTACCTTTACACTGGCTTGAA	1431

RESULT 15

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; GENERAL INFORMATION:

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; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

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; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match 45.5%; Score 516; DB 11; Length 1335;
Best Local Similarity 70.2%; Pred. No. 2.3e-138;
Matches 709; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

Qy	80	ATGAAGATGAGTTCTCCGCTATCTGTGGCGTATTATCTGTACCCAAAACAGTATGAGT	139
Db	104	ACGACGAGGAATTCTGCCTGCGGTACCTGTGGAGGGAAATACCTGCACCCGAAAGAATATGAGT	163
Qy	140	GGGTCCCTCATCGCAGCCTATGTGGCTGTGTCGTCGTGCCCTGGTGGCAACACGCTGG	199
Db	164	GGGTCCCTGATGCCGGGTACATCATCGTGTCGTCGTGGCTCTCATTGGAACGTCCTGG	223
Qy	200	TCTGCCTGGCCGTGTGGCGAACACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	224	TTTGTGTGGCAGTGTGGAAGAACCAACCATGAGGACGGTAACCAACTACTTCATAGTCA	283
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTACTGCTATCTGCCTGCCGCCAGCCTGCTGGTGG	319
Db	284	ATCTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG	343
Qy	320	ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTATCCCCTATCTACAGG	379
Db	344	ATATCACTGAGACCTGGTTTTGGACAGTCCTTGCAGGTGATTCTTATCTACAGA	403
Qy	380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATGCCCTGGACCGCTGGTATG	439
Db	404	CCGTGTCCGTGTCAGTGGCTGTCACACTGAGCTGATGCCCTGGATCGGTGGTATG	463
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGGCCGTGGCTCCATCCTGG	499
Db	464	CAATCTGTCACCCTTGATGTTAACAGAGCACAGCAAAGCGGGCCGTAACAGCATTGTCA	523
Qy	500	GCATCTGGCTGTGCGCTGCCATCATGGTCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	524	TCATCTGGATTGTCCTGCATTATAATGATTCTCAGGCCATCGTCATGGAGTGCAGCA	583
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTCTCAGTCTGTGATGAACGCTGGG	619
Db	584	CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCCTTTACGGTGTGATGAGCGCTGGG	643
Qy	620	CAGATGACCTCTATCCAAGATCTACCACAGTTGCTTCTTATTGTCACCTACCTGGCCC	679
Db	644	GTGGTGAATTATCCAAGATGTACCACATCTGTTCTTCTGGTACATACATGGCAC	703
Qy	680	CACTGGGCCTCATGCCATGGCTATTCCAGATATTCCGCAAGCTCTGGGGCCAGA	739

Db 704 CACTGTGTCATGGTGGCTTATCTGCAAATATTGCAAACTCTGGTGTGACAGA 763 .
Qy 740 TCCCCGGCACCCACCTCAGCACTGGTGCAGGAACCTGGAAGCGCCCTCAGACCAGCTGGGG 799
Db 764 TCCCTGGAACATCATCTGTAGTTAGAGAAAATGGAAGCCCC-----TGCAGCCTGTT 817
Qy 800 ACCTGGAGCAGGGCTGAGTGGAGAGCCCCAGCCCCGGGCCGCCTTCCTGGCTGAAG 859
Db 818 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCCGATGAGCGCTGTGGCGCTGAAA 877
Qy 860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
Db 878 TAAAGCAGATCCGAGGCCAGAAGAAAACAAACGGATGTTGATGGTTGTGCTTTGGTAT 937
Qy 920 TCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGGCTGGGATGT 979
Db 938 TTGCAATTGCTATCTACCAATTAGCATCCTCAATGTCCTAAAGAGAGTATTGGGATGT 997
Qy 980 TCCGCCAACGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTCACCTTCTCCACTGGCTGG 1039
Db 998 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCCTGGTTACCTTTCACACTGGCTTG 1057
Qy 1040 TGTACGCCAACAGCGCTGCCAACCCATCATCTACAACCTCCTCAGTGG 1089
Db 1058 TATATGCCAATAGTGCCTGCGAATCCAATTATTTATAATTCTCAGTGG 1107

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